

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:43:04 ; Search time 39.63 Seconds
(without alignments)
52.383 Million cell updates/sec

Title: US-09-461-061A-2

Perfect score: 60

Sequence: 1 TLHWTITKLNAE 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	23	38.3	8	2 Q45615	Q45615 bacillus su
2	22	36.7	11	8 O79921	O79921 phrynoceph
3	20.5	34.2	10	6 Q9TRU6	Q9TRU6 bos taurus
4	18	30.0	7	2 Q54248	Q54248 streptomyce
5	18	30.0	8	3 Q05403	Q05403 saccharomyc
6	18	30.0	9	4 Q14277	Q14277 homo sapien
7	18	30.0	10	6 Q9XS84	Q9XS84 equus cabal
8	18	30.0	11	5 Q9VN99	Q9VN99 drosophila
9	17	28.3	8	2 P83158	P83158 anabaena sp
10	17	28.3	10	11 Q91WZ3	Q91WZ3 rattus sp.
11	17	28.3	11	8 Q94VK1	Q94VK1 varanus aca
12	17	28.3	11	8 Q94V88	Q94V88 varanus gou
13	17	28.3	11	8 Q94VE7	Q94VE7 varanus kom
14	17	28.3	11	8 Q94VB8	Q94VB8 varanus sal
15	17	28.3	11	9 Q37925	Q37925 bacterioph
16	17	28.3	12	2 Q50342	Q50342 mycoplasma

17	17	28.3	12	11 Q9WUX1	Q9WUX1 rattus norv
18	17	28.3	12	16 Q9K670	Q9K670 bacillus ha
19	16	26.7	7	2 P72081	P72081 nocardia la
20	16	26.7	8	4 Q15889	Q15889 homo sapien
21	16	26.7	9	4 QH4M8	QH4M8 homo sapien
22	16	26.7	9	12 P90359	P90359 barley mild
23	16	26.7	10	8 Q9TGA1	Q9TGA1 heloderma s
24	16	26.7	10	8 Q9TG98	Q9TG98 shinisauru
25	16	26.7	10	8 Q9TGA3	Q9TGA3 diploglossu
26	16	26.7	10	8 Q9TGA7	Q9TGA7 sauresia ag
27	16	26.7	10	8 Q9TGA4	Q9TGA4 weimorena h
28	16	26.7	10	8 Q9TGA4	Q9TGA4 anguis frag
29	16	26.7	10	8 Q9TGA4	Q9TGA4 anguis frag
30	16	26.7	10	8 Q9TGA4	Q9TGA4 anguis frag
31	16	26.7	10	8 Q9TGA4	Q9TGA4 anguis frag
32	16	26.7	10	8 Q9TGA4	Q9TGA4 anguis frag
33	16	26.7	11	7 Q77884	Q77884 oreochromis
34	16	26.7	11	7 Q77885	Q77885 oreochromis
35	16	26.7	11	8 Q94V77	Q94V77 heloderma s
36	16	26.7	12	2 P83054	P83054 bacteroides
37	16	26.7	12	3 Q9UR22	Q9UR22 cryptococcu
38	15	25.0	7	2 Q47029	Q47029 equine infe
39	15	25.0	8	2 Q47029	Q47029 enterobacte
40	15	25.0	8	2 Q47029	Q47029 enterobacte
41	15	25.0	8	6 Q9TT78	Q9TT78 canis famil
42	15	25.0	9	2 Q47556	Q47556 escherichia
43	15	25.0	9	2 Q51349	Q51349 pseudomonas
44	15	25.0	10	2 Q9F5W1	Q9F5W1 vibrio chol
45	15	25.0	10	5 P82223	P82223 bombyx mori

ALIGNMENTS

RESULT 1					
Q45615	PRELIMINARY;	PRT;	8 AA.		
AC Q45615;					
DT 01-NOV-1996 (TREMREL. 01, Created)					
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)					
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)					
DE GUTB PROTEIN (FRAGMENT).					
GN GUTB.					
OS Bacillus subtilis.					
OC Bacteria; Firmicutes; Bacillus/Clostridium group;					
OC Bacillus/Staphylococcus group; Bacillus.					
ON NCBI_TaxID=1423;					
RX [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=168;					
RX MEDLINE=94253000; PubMed=8195086;					
RA Ye R., Wong S.L.;					
RT "Transcriptional regulation of the Bacillus subtilis glucitol					
RT dehydrogenase gene.";					
RL J. Bacteriol. 176:3314-3320(1994).					
DR EMBL; L16626; AAA20875.1; -					
FT NON_TER 8					
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;					

Query Match 38.3%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHTI 6
Db 1 MTHTV 5

RESULT 2
O79921 PRELIMINARY; PRT; 11 AA.
ID O79921
AC O79921;

```
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI
OS Phrynocephalus raddai.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agamini;
OC Phrynocephalus.
OX NCBI_TaxID=52206;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97315309; PubMed=9169559;
RX Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT mitochondrial genome among iguanian lizards.";
RL J. Mol. Evol. 44:660-674(1997).
DR EMBL; U82691; AAC62302.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1324 MW; 5DF73710D371F1A7 CRC64;

Query Match 36.7%; Score 22; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLTH 4
Db 3 TLTH 6

RESULT 3
Q9TRU6 PRELIMINARY; PRT; 10 AA.
AC Q9TRU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE GAP-3, GTPASE-ACTIVATING PROTEIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92112868; PubMed=1309786;
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol.";
RL J. Biol. Chem. 267:1546-1553(1992).
SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 34.2%; Score 20.5; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 6 ITKL-NAE 12
Db 3 LTKLTNAE 10

RESULT 4
Q54248 PRELIMINARY; PRT; 7 AA.
AC Q54248;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE RET PROTEIN SHORT FORM (FRAGMENT).
OS Homo sapiens (Human).
```

```
DE RPLO PROTEIN (FRAGMENT).
GN RPLO.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the sec Y protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 30.0%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TITKL 9
Db 2 TVTEL 6

RESULT 5
Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DNA FOR ORF S FROM CHROMOSOME XV (FRAGMENT).
GN COQ3 AND YOL096C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumstein E., Pearson B.M., Kalođeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
DR SGD; S0005456; COQ3.
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 30.0%; Score 18; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HTTKL 9
Db 3 HNVVKI 8

RESULT 6
Q14277 PRELIMINARY; PRT; 9 AA.
AC Q14277;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE RET PROTEIN SHORT FORM (FRAGMENT).
OS Homo sapiens (Human).
```

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=94071887; PubMed=7902707;
RX	Ceccherini I., Boccardi R., Luo Y., Pasini B., Hofstra R.,
RA	Takahashi M., Romeo G.;
RA	"Exon structure and flanking intronic sequences of the human RET
RT	proto-oncogene.";
RT	Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
RL	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94366753; PubMed=8084609;
RA	Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
RA	Boccardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
RA	Bozzano M., Buys C., Romeo G.;
RT	"DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
RT	the ret proto-oncogene.";
RT	Oncogene 9:3023-3029(1994).
DR	EMBL; U11532; AAC50102.1; -.
FT	NON_TER 1
FT	1
SEQ	SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;
Query Match 30.0%; Score 18; DB 4; Length 9;	
Best Local Similarity 28.6%; Pred. No. 5.6e+05;	
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	2 LTHYTIK 8
DB	::: :
DB	2 ISHAFT 8
RESULT 7	
Q9XS84	
ID	Q9XS84 PRELIMINARY; PRT; 10 AA.
AC	Q9XS84;
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	LEPTIN (FRAGMENT).
GN	LEP.
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;	
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=99160468; PubMed=10051323;
RA	Caetano A.R., Pomp D., Murray J.D., Bowling A.T.;
RT	"Comparative mapping of 18 equine type I genes assigned by somatic
RT	cell hybrid analysis.";
RL	Mamm. Genome 10:271-276(1999).
DR	EMBL; AF097582; AAD25985.1; -.
FT	NON_TER 1
FT	1
FT	NON_TER 10 10
SEQ	SEQUENCE 10 AA; 1155 MW; 6BE77BB05AA44044 CRC64;
Query Match 30.0%; Score 18; DB 6; Length 10;	
Best Local Similarity 40.0%; Pred. No. 6.2e+03;	
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	
QY	6 ITKLN 10
DB	::: :
DB	1 VTRIN 5
RESULT 8	
Q9VN99	
ID	Q9VN99 PRELIMINARY; PRT; 11 AA.
AC	Q9VN99;

DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE	CG2676 PROTEIN.
DN	CG2676.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hosdin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Swigas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster.";
RL	Science 287:2185-2195(2000).
DR	EMBL; AE003603; AAF52049.1;
DR	FlyBase; FBgn0037309; CG2676.
RS	SEQUENCE 11 AA; 1113 MW; 8760FE9BD5A1B1B1 CRC64;
QY	2 LTHTTTKNAE 12
DB	1 MTATTSVSSK 11
RESULT	9
P83158	PRELIMINARY; PRT; 8 AA.
ID	P83158
AC	P83158;
DT	01-DEC-2001 (TReMBLrel. 19, Created)
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KDA
DE POLYPEPTIDE) (PSI-C) (FRAGMENT).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC !- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
CC PHOTOSYSTEM I COMPLEX.
CC !- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC !- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4Fe-4S FERREDOXINS.
DR InterPro: IPR001450; 4Fe4S ferredoxin.
DR PROSITE: PS00198; 4FE4S.FERREDOXIN; PARTIAL.
KW Photosynthesis; Photosystem I; Iron sulfur; 4Fe-4S; Metal-binding.
FT NON_TER 8
SQ SEQUENCE 8 AA; 962 MW; C5BB505322D1A1F5 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.6e+05; Indels 0; Gaps 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 THTI 6
Db 1 SHTV 4

RESULT 10
Q91WZ3
ID Q91WZ3 PRELIMINARY; PRT; 10 AA.
AC Q91WZ3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE LUTEINIZING HORMONE/CHORIONIC GONADOTROPIN RECEPTOR HOMOLOG
DE (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen O.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL; S80660; AAB50710.1; -.
KW Receptor; Chorion.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;

Query Match 28.3%; Score 17; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTH 4
Db 8 LTH 10

RESULT 11
Q94VK1
ID Q94VK1 PRELIMINARY; PRT; 11 AA.
AC Q94VK1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus acanthurus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62035;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407488; AAL10021.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 28.3%; Score 17; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+04; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLTHITIKLN 10
Db 2 TLTRWLFSTN 11

RESULT 12
Q94VG8
ID Q94VG8 PRELIMINARY; PRT; 11 AA.
AC Q94VG8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus gouldii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62042;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407502; AAL10060.1; -.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 28.3%; Score 17; DB 8; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.1e+04; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLTHITIKLN 10
Db 2 TLTRWLFSTN 11

RESULT 13
Q94VE7
ID Q94VE7 PRELIMINARY; PRT; 11 AA.
AC Q94VE7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus komodoensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodonta; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407510; AAL10084.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 11 AA; 1370 MW; 8E6DE80C7336411 CRC64;

Query Match 28.3%; Score 17; DB 8; Length 11;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLTHITITKLN 10
 DB 2 TLTRWLFSTN 11

RESULT 14
 Q94VB8
 ID Q94VB8 PRELIMINARY; PRT; 11 AA.
 AC Q94VB8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
 GN COI.
 OS Varanus salvadorii.
 OG Mitochondrion.
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407522; AAL10119.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 11 AA; 1370 MW; 8E6DE80C7336411 CRC64;

Query Match 28.3%; Score 17; DB 8; Length 11;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLTHITITKLN 10
 DB 2 TLTRWLFSTN 11

RESULT 15
 Q37925
 ID Q37925 PRELIMINARY; PRT; 11 AA.
 AC Q37925;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE BACTERIOPHAGE FR REPLICASE (FRAGMENT).
 OS Bacteriophage fr.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Berzin V.M.; Gribanov V.A.; Cielens I.E.; Jansone I.V.; Gren E.J.;
 RT "The nucleotide sequence of the regulatory region of phage fr
 apicase cistron.";

RL Bioorg. Khim. 7:306-308(1981).
 DR EMBL; M34834; AAA32193.1; -.
 FT NON_TER
 SQ SEQUENCE 11 AA; 1265 MW; 8BD43470C33321B1 CRC64;

Query Match 28.3%; Score 17; DB 9; Length 11;
 Best Local Similarity 30.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 LTHITITKLN 11
 DB 1 MSKTKKFN 10

RESULT 16
 Q50342
 ID Q50342 PRELIMINARY; PRT; 12 AA.
 AC Q50342;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE ATP-SYNTHASE ALPHA (FRAGMENT).
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-M129;
 RX MEDLINE-95075318; PubMed-7984111;
 RT "Identification and Characterization of hitherto unknown Mycoplasma
 pneumoniae proteins.";
 RL Mol. Microbiol. 13:337-348(1994).
 DR EMBL; Z32665; CAA83583.1; -.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1396 MW; 8A7DE4E61CA1A681 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLTHIT 5
 DB 3 TLTHIT 7

RESULT 17
 Q9WUX1
 ID Q9WUX1 PRELIMINARY; PRT; 12 AA.
 AC Q9WUX1;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE APOBEC-1 PROTEIN (FRAGMENT).
 GN APOBEC-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98335789; PubMed-9672068;
 RA Greeve J.; Axelos D.; Welker S.; Schipper M.; Greden H.;
 RT "Distinct promoters induce APOBEC-1 expression in rat liver and
 intestine.";
 RL Arterioscler. Thromb. Vasc. Biol. 18:1079-1092(1998).
 DR EMBL; AJ006695; CAB44439.1; -.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1357 MW; 70FB1679699325BB CRC64;

1 8 11:37:00 2002

Query Match 26.7%; Score 16; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 5.6e+05; Indels 0;
Matches 2; Conservative 1; Mismatches 1; Gaps 0;

QY 4 HTIT 7
Db 3 HAVT 6

RESULT 20
Q15889 PRELIMINARY; PRT; 8 AA.

ID Q15889
AC Q15889
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CLONE XP15H8B (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32070; AAA73879.1;
FT NON_TER 1
FT SEQUENCE 8 AA; 865 MW; 04744732325A761E7 CRC64;

Query Match 26.7%; Score 16; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TKLN 10
Db 4 SKLN 7

Search completed: July 8, 2002, 11:48:39
Job time: 335 sec

Query Match 28.3%; Score 17; DB 11; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.2e+04; Indels 0;
Matches 3; Conservative 4; Mismatches 1; Gaps 0;

QY 5 TITKLN 12
Db 4 TESKMSSE 11

RESULT 18
Q9K670 PRELIMINARY; PRT; 12 AA.

ID Q9K670
AC Q9K670
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE BH3862 PROTEIN.
GN BH3862.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OC NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11059132;
RA Takami H., Nakasone K., Takaki Y., Ogasawara N., Kuhara S.,
RA Fuji F., Hirama C., Nakamura Y.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001520; BAB07581.1;
FT COMPLETE PROTEOME.
SQ SEQUENCE 12 AA; 1463 MW; 44E501F9695321A7 CRC64;

Query Match 28.3%; Score 17; DB 16; Length 12;
Best Local Similarity 25.0%; Pred. No. 1.2e+04; Indels 0;
Matches 2; Conservative 4; Mismatches 2; Gaps 0;

QY 2 LPHITITKL 9
Db 1 MNVLLTKI 8

RESULT 19
P72081 PRELIMINARY; PRT; 7 AA.

ID P72081
AC P72081
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 3'-METHYLCEPHEM HYDROXYLASE (FRAGMENT).
GN CEF.
OS Nocardia lactamdurans.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OC NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis."
RL Gen. 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1;
FT NON_TER 1
SQ SEQUENCE 3, 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:44:04 ; Search time 12.97 Seconds
(without alignments)
60.264 Million cell up

Title: US-09-461-061A-4

Perfect score: 161

Sequence: 1 TLTHITKLNAENNATFYFKIDNVKKARQVW 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs. 24425594 residues

Total number of hits satisfying chosen parameters: 146970

Minimum DB seq length: 0

Minimum DB	seq	length:	0
Maximum DB	seq	length:	32

maximum DB seq length: 32

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pe

6: /cgn2_6/ptodata/2/iaa/backfiles1.pe

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	95	59.0	32	4	US-08-676-242-15	Sequence 15, Appl	
2	41	25.5	26	1	US-07-946-421-17	Sequence 17, Appl	
3	39	24.2	31	2	US-08-318-157B-28	Sequence 28, Appl	
4	39	24.2	32	1	US-07-946-421-9	Sequence 9, Appl	
5	39	24.2	32	1	US-08-137-117D-122	Sequence 122, App	
6	39	24.2	32	1	US-08-137-117D-124	Sequence 124, App	
7	39	24.2	32	1	US-08-137-117D-141	Sequence 141, App	
8	39	24.2	32	2	US-08-436-717-122	Sequence 122, App	
9	39	24.2	32	2	US-08-436-717-124	Sequence 124, App	
10	39	24.2	32	2	US-08-436-717-141	Sequence 141, App	
11	39	24.2	32	2	US-08-553-501A-67	Sequence 67, Appl	
12	39	24.2	32	2	US-08-553-501A-71	Sequence 71, Appl	
13	39	24.2	32	2	US-08-560-558E-3	Sequence 3, Appl	
14	39	24.2	32	2	US-08-763-783A-89	Sequence 89, Appl	
15	39	24.2	32	2	US-08-765-783A-91	Sequence 91, Appl	
16	39	24.2	32	3	US-09-205-231-67	Sequence 67, Appl	
17	39	24.2	32	3	US-09-205-231-71	Sequence 71, Appl	
18	39	24.2	32	4	US-08-646-265A-123	Sequence 123, App	
19	39	24.2	32	4	US-09-416-557-89	Sequence 89, Appl	
20	39	24.2	32	4	US-09-416-557-91	Sequence 91, Appl	
21	37	23.0	20	2	US-08-053-451B-169	Sequence 169, App	
22	37	23.0	32	2	US-08-470-139-13	Sequence 13, Appl	
23	37	23.0	32	4	US-08-569-147-40	Sequence 40, Appl	
24	37	23.0	32	4	US-09-347-061-13	Sequence 13, Appl	
25	37	23.0	32	4	US-09-425-638A-92	Sequence 92, Appl	
26	37	23.0	32	4	US-09-425-638A-93	Sequence 93, Appl	
27	37	23.0	32	4	US-09-425-638A-94	Sequence 94, Appl	

ALIGNMENTS

RESULT 1

```

US-08-676-242-15
; Sequence 15, Application US/08676242C
; Patent No. 6143719
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of Michigan
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Hasan, Ahmed A.K.
; TITLE OF INVENTION: Bradykinin Analogs As Selective
; FILE REFERENCE: 8820-2 US
; CURRENT APPLICATION NUMBER: US/08/676,242C
; CURRENT FILING DATE: 2000-07-16
; EARLIER APPLICATION NUMBER: 60/000,096
; EARLIER FILING DATE: 1995-06-09
; EARLIER APPLICATION NUMBER: PCT/US96/09940
; EARLIER FILING DATE: 1996-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: analog
US-08-676-242-15

```

Query Match 59.0%; Score 95; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels

QY 14 NATFYFKIDNVKKARQVV 32
|||||

D6 1 NATFYFKIDNVKKARQVV 19

RESULT

2
 US-07-946-421-17
 ; Sequence 17, Application US/07946421
 ; Patent No. 5558864
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Kettleborough, Catherine A.
 ; APPLICANT: Saidanha, Jose
 ; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
 ; TITLE OF INVENTION: Antibodies
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-07-946-421-17

Query Match 25.5%; Score 41; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TITKLNAENNAFFY 18
||::||:|::|

Db 18 TISRMEADAATYY 31

RESULT 3

US-08-318-157B-28
Sequence 28, Application US/08318157B
Patent No. 5674540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "At site 4, Xaa = Ser or
OTHER INFORMATION: Asp."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "At site 9, Xaa = Gly or
OTHER INFORMATION: Val."
US-08-318-157B-28

Query Match 24.2%; Score 39; DB 2; Length 31;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNAFFY 18
|::|:|:|:|

Db 15 TFTISLQPEDATYY 30

RESULT 4

US-07-946-421-9
Sequence 9, Application US/07946421
Patent No. 5558864
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saidanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Region
; LOCATION: 15
; OTHER INFORMATION: /note= "Amino acid 15 can be Tyr,
; OTHER INFORMATION: Phe, Trp or His."
; US-07-946-421-9

Query Match 24.2%; Score 39; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

QY 3 THTITKLNNAENNAFFY 18
| | | | | : | | : | | : |
Db 16 TFISSLPQEDIAFY 31

RESULT 5
US-08-137-117D-122
; Sequence 122, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JF92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-137-117D-122

Query Match 24.2%; Score 39; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNNAENNAFFY 18
| | | | | : | | : | | : |
Db 16 TFISSLPQEDIAFY 31

RESULT 6
US-08-137-117D-124
; Sequence 124, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JF92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-137-117D-124

Query Match 24.2%; Score 39; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNNAENATFY 18
| | | | | | | | | |
Db 16 TFTISSLPEDIATY 31

RESULT 7

US-08-137-117D-141
; Sequence 141, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-137-117D-141

Query Match 24.2%; Score 39; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNNAENATFY 18
| | | | | | | | | |
Db 16 TFTISSLPEDIATY 31

RESULT 8

US-08-436-717-122

; Sequence 122, Application US/08436717
; Patent No. 5817790

; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-717-122

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNNAENATFY 18
| | | | | | | | | |
Db 16 TFTISSLPEDIATY 31

RESULT 9

US-08-436-717-124
; Sequence 124, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-124

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

Qy 3 THTTIKLNAENNATFY 18
| | | | | | | | | |
Db 16 TFTTISLQPEDATYV 31

RESULT 10

US-08-436-717-141
Sequence 141, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-141

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

Qy 3 THTTIKLNAENNATFY 18
| | | | | | | | | |
Db 16 TFTTISLQPEDATYV 31

RESULT 11

US-08-553-501A-67
Sequence 67, Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-553-501A-67

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATFY 18
| ||: | | : ||: |
Db 16 TFTISSLOPEDIATYY 31

RESULT 12
US-08-553-501A-71
; Sequence 71, Application US/08553501A
; Patent No. 5856135
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-553-501A-71

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATFY 18
| ||: | | : ||: |
Db 16 TFTISSLOPEDIATYY 31

RESULT 13
US-08-560-558E-3
; Sequence 3, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: United States of America
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: WordPerfect 5.1/5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,558E
; FILING DATE: No. 5891996ember 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 27200S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-560-558E-3

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATFY 18
| ||: | | : ||: |
Db 16 TFTISSLOPEDIATYY 31

RESULT 14
US-08-765-783A-89
; Sequence 89, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-89

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTTKLNAENNAIFY 18
Db 16 TFTISSLPEDIATYY 31

RESULT 15
US-08-765-783A-91
; Sequence 91, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-89

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTTKLNAENNAIFY 18
Db 16 TFTISSLPEDIATYY 31

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-765-783A-91

Query Match 24.2%; Score 39; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTTKLNAENNAIFY 18
Db 16 TFTISSLPEDIATYY 31

RESULT 16
US-09-205-231-67
; Sequence 67, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-205-231-67

Query Match 24.2%; Score 39; DB 3; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKNAENNATFY 18
| ||: | | : ||: |
Db 16 TFTISSLPEDIATYV 31

RESULT 17
US-09-205-231-71
; Sequence 71, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yulchi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-205-231-71

Query Match 24.2%; Score 39; DB 3; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKNAENNATFY 18
| ||: | | : ||: |
Db 16 TFTISSLPEDIATYV 31

RESULT 18
US-08-646-265A-123
; Sequence 123, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-123

Query Match 24.2%; Score 39; DB 4; Length 32;

Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THHTITKLNAENNATFY 18
| | | | | | | | | |
Db 16 TFTTSSLPEDIATYY 31

RESULT 19

US-09-416-557-89
; Sequence 89, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,557
; FILING DATE: 12-October-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,783
; FILING DATE: 7-March-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-416-557-89

Query Match 24.2%; Score 39; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THHTITKLNAENNATFY 18
| | | | | | | | | |
Db 16 TFTTSSLPEDIATYY 31

RESULT 20

US-09-416-557-91
; Sequence 91, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji

; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,557
; FILING DATE: 12-October-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,783
; FILING DATE: 7-March-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-416-557-91

Query Match 24.2%; Score 39; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THHTITKLNAENNATFY 18
| | | | | | | | | |
Db 16 TFTTSSLPEDIATYY 31

Search completed: July 8, 2002, 11:49:17
Job time: 313 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:39:08 ; Search time 48.86 Seconds
(without alignments)
27.280 Million cell updates/sec

Title: US-09-461-061A-2
Perfect score: 60
Sequence: 1 TLTHTTKLNAE 12

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 158732

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*

1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	12	21 AAY95406	Anti-angiogenic pe
2	30	50.0	10	22 AAJ01502	Hepatitis C virus
3	27	45.0	10	22 AAG96132	Human complementar
4	27	45.0	10	22 AAG84421	Arabidopsis thalia
5	26	43.3	9	16 AAR61413	TNF-alpha related
6	26	43.3	9	19 AAW58653	Platelet factor 4
7	26	43.3	11	16 AAR87682	h-TNF (70-80). Sy
8	26	43.3	11	16 AAR87684	h-TNF (70-80) anal
9	26	43.3	11	21 AAY52581	Anarthus viridis
10	26	43.3	12	18 AAY35497	TNF alpha peptide
11	25	41.7	9	20 AAY46762	Immunogenic peptid

12	24	40.0	8	22	AAG89420	p53 DR supermotif
13	24	40.0	8	22	AAG89421	p53 DR supermotif
14	24	40.0	10	18	AAW30080	Hamster neuritin
15	24	40.0	10	18	AAW13715	Internal neuritin
16	24	40.0	10	20	AAW16636	W0914235 Seq ID N
17	24	40.0	10	22	AAW42846	Myocoplama genital
18	24	40.0	11	16	AAR87683	h-TNF (70-80) anal
19	24	40.0	11	18	AAW54449	Cytokine derived p
20	24	40.0	11	19	AAW47911	Human tumour necro
21	24	40.0	11	19	AAW47912	Human tumour necro
22	24	40.0	11	19	AAW47916	Human tumour necro
23	24	40.0	11	19	AAW47917	Human tumour necro
24	24	40.0	11	19	AAW47918	Human tumour necro
25	24	40.0	11	19	AAW47922	Human tumour necro
26	24	40.0	11	19	AAW47900	Human tumour necro
27	24	40.0	11	19	AAW47901	Human tumour necro
28	24	40.0	11	19	AAW47903	Human tumour necro
29	24	40.0	11	19	AAW47904	Human tumour necro
30	24	40.0	11	19	AAW47876	Human tumour necro
31	24	40.0	11	19	AAW47877	Human tumour necro
32	24	40.0	11	19	AAW47860	Human tumour necro
33	24	40.0	11	19	AAW47865	Human tumour necro
34	24	40.0	11	19	AAW47863	Human tumour necro
35	24	40.0	11	19	AAW47868	Human tumour necro
36	24	40.0	11	19	AAW47869	Human tumour necro
37	24	40.0	11	19	AAW47870	Human tumour necro
38	24	40.0	11	19	AAW47871	Human tumour necro
39	24	40.0	11	19	AAW47872	Human tumour necro
40	24	40.0	11	19	AAW47873	Human tumour necro
41	24	40.0	11	19	AAW47874	Human tumour necro
42	24	40.0	11	19	AAW47875	Human tumour necro
43	24	40.0	11	22	AAW84078	Immune modulating
44	24	40.0	12	19	AAW47910	Human tumour necro
45	24	40.0	12	19	AAW47892	Human tumour necro

ALIGNMENTS

RESULT 1

AAW95406

ID AAY95406 standard; Peptide; 12 AA.

AC AAY95406;

DT 25-SEP-2000 (first entry)

DE Anti-angiogenic peptide N-terminal fragment.

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

OS Homo sapiens.

PN WO200035407-A2.

PD 22-JUN-2000.

PF 02-DEC-1999; 99WO-US28465.

PR 16-DEC-1998; 98US-0112427.

PA (UTEM) UNIV TEMPLE.

PA (MCCR/) MCCRAE R K.

PI McCrae RK;

DR WPI; 2000-442247/38.

PT Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer,

PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog -
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The present sequence is that of an N-terminal fragment of a novel
CC anti-angiogenic D3 peptide (see AAY95408) derived from human high
CC mol.wt. kininogen (HK) domain 3 (see AAY95426). The full-length D3
CC peptide inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of peptides of the
CC invention (see AAY95405-26) that are analogues of certain sites in
CC the HK domain 3. The peptides inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 60; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLTHITKINAE 12
Db 1 tlthitkinae 12
|||||

RESULT 2
AAJ01502
ID AAJ01502 standard; Peptide; 10 AA.
XX
AC AAJ01502;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #1493.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX
PA (EPTM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccine against hepatitis C virus -
XX
PS Disclosure; Page 138; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans.
CC The present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 10 AA;

Query Match 50.0%; Score 30; DB 22; Length 10;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TLTHITK 8
Db 1 tlthpitk 7
||| |||

RESULT 3
AAG96132
ID AAG96132 standard; Peptide; 10 AA.
XX
AC AAG96132;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 2326.
XX
KW Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04776.
XX
PR 13-DEC-1999; 99GB-0029464.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-408419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
PS Example 4; Page 375; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;

Query Match 45.0%; Score 27; DB 22; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLTHITK 9
Db 2 tathslsrl 10
| ||::||

RESULT 4
AAG84421
ID AAG84421 standard; Peptide; 10 AA.
XX
AC AAG84421;
XX
DT 11-SEP-2001 (first entry)
XX
DE Arabidopsis thaliana peptide ligand #1061.

XX Plant; peptide pesticide; peptide herbicide; agricultural research.
KW Arabidopsis thaliana.
OS WO200142279-A2.
XX PN 14-JUN-2001.
XX PD 13-DEC-2000; 2000WO-GB04781.
XX PF 13-DEC-1999; 99GB-0029469.
XX PR (PROT-) PROTEOM LTD.
XX PA Roberts GW, Heal JR;
XX PI WPI; 2001-381629/40.
XX DR A set of peptide ligands for agricultural research and development of
XX PT therapeutic agents comprise specific complementary peptides to proteins
XX PT encoded by genes of plant genomes -
XX PS Example 4; Page 179; 201pp; English.
XX CC The present invention relates to a set of peptide ligands consisting of
XX CC specific complementary peptides to proteins encoded by genes of plant
XX CC genomes. The present sequence is one such peptide from Arabidopsis
XX CC thaliana. The peptides of the present invention are useful in an assay to
XX CC identify a peptide, especially a peptide pesticide or herbicide. The
XX CC peptides are also useful for tools for agricultural research and
XX CC development.
XX SQ Sequence 10 AA;

Query Match 45.0%; Score 27; DB 22; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLTHITK 8
Db 3 tlqtlrk 10

RESULT 5
ID AAR61413 standard; peptide; 9 AA.
XX AC AAR61413;
XX DT 25-AUG-1995 (first entry)
XX DE TNF-alpha related peptide designated CT-119.
XX KW antiinflammatory; platelet factor 4; PF-4 autoimmune disease;
XX KW graft-versus-host; reperfusion injury; atherosclerosis; asthma.
XX OS Synthetic.
XX PN WO9500543-A.
XX PD 05-JAN-1995.
XX PF 17-JUN-1994; 94WO-US06888.
XX PR 18-JUN-1993; 93US-0080371.
XX PA (COUNT) COUNTS D F.
XX PA (DUFF) DUFF R G.
XX PI Counts DF, Duff RG;
XX

DR WPI; 1995-052005/07.
XX New peptide(s) and derivs. based on platelet factor 4 - used for
XX PT inhibiting an immune response, including an inflammatory response
XX PT in e.g. autoimmune diseases.
XX PS Disclosure; Page 38; 99pp; English.
XX CC New peptides are disclosed which include any peptide, peptide
XX CC derivative or peptide analogue which comprises either (i) at least a
XX CC 4 amino acid portion of PF-4 (see AAR61401) or a functionally equivalent
XX CC sequence, or (ii) at least a 6 amino acid sequence which is at least
XX CC 66% homologous to a portion of the PF-4 sequence, or a functionally
XX CC equivalent sequence. Pref. the peptide contains the sequence
XX CC Thr-Ser-Gln and/or Val-Arg-Pro, and more preferably Thr-Thr-Ser-Gln
XX CC Thr-Thr-Ser-Gln-Val-Arg-Pro-Arg (AAR61393), designated CT-112.
XX CC The peptide may be derivatised at the N- and/or C-terminal, or may be
XX CC cyclised, substituted, truncated or contain D-amino acid residues.
XX CC The peptides exhibit antiinflammatory activity and may be used to treat
XX CC autoimmune diseases (such as insulin-dependent diabetes, ulcerative
XX CC colitis, rheumatoid arthritis, scleroderma, mixed connective tissue
XX CC disease and SLE), reperfusion tissue damage, inflammatory lung disease,
XX CC graft-versus-host disease, atherosclerosis and asthma.
XX CC The present sequence, designated CT-119, is a comparison sequence
XX CC from TNF-alpha, constructed for testing and comparison purposes.
XX CC When tested for antiinflammatory activity by the mouse ear acute
XX CC inflammation model at a dose of 60 mg/kg administered gradually
XX CC over 24 hr, the peptide CT-112 gave an inhibition of 78%. In
XX CC comparison the present sequence gave a value of 74%.
XX SQ Sequence 9 AA;

Query Match 43.3%; Score 26; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
Db 5 lthtl 9

RESULT 6
AAW58653
ID AAW58653 standard; peptide; 9 AA.
XX AC AAW58653;
XX DT 08-SEP-1998 (first entry)
XX DE Platelet factor 4 derived peptide SEQ ID NO:21 CT-119.
XX KW Platelet factor 4; PF4; anti-inflammatory; inhibition; inflammation;
XX KW autoimmune disease; graft versus host disease; reperfusion injury;
XX KW atherosclerosis; asthma; chemokine.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US5776892-A.
XX PD 07-JUL-1998.
XX PF 16-JUN-1994; 94US-0250550.
XX PR 16-JUN-1994; 94US-0259550.
XX PR 21-DEC-1990; 90US-0631823.
XX PR 24-MAR-1993; 93US-0037486.
XX PR 18-JUN-1993; 93US-0080371.
XX PA (CURA-) CURATIVE HEALTH SERVICES INC.
XX

PI Counts DF, Duff RG;
XX WPI; 1998-398086/34.
XX
XX New antiinflammatory peptide(s) based on platelet factor 4 sequences
PT - used for treating e.g. autoimmune diseases, graft versus host
PT disease, reperfusion injury, atherosclerosis or asthma
XX
XX Example 14; Column 21; 55pp; English.
XX
XX The present sequence represents a peptide which is related to platelet
CC factor 4 (PF4) and can be used to inhibit an inflammatory response.
CC Peptides, peptide analogues and peptide derivatives of PF4 can be used
CC for treating e.g. autoimmune diseases such as insulin dependent
CC diabetes, Goodpasture's syndrome, pemphigus and pemphigoid, primary
CC biliary cirrhosis, ulcerative colitis, rheumatoid arthritis,
CC scleroderma, mixed connective tissue disease and lupus erythematosus,
CC graft versus host disease, septic shock, reperfusion injury (including
CC injury subsequent to myocardial or cerebral infarction),
CC atherosclerosis, asthma and inflammatory lung disease. The peptides
CC give a new and effective method of inhibiting the inflammatory response
CC by acting on cytokines rather than the prior art arachidonic acid.
XX
XX Sequence 9 AA;

Query Match 43.3%; Score 26; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHTI 6
Db | | | |
5 ltht1 9

RESULT 7
AAR87682
ID AAR87682 standard; peptide; 11 AA.

AC AAR87682;

DT 10-MAY-1996 (first entry)

DE h-TNF (70-80).

XX TNF; tumour necrosis factor; neutrophil; superoxide; inflammation;
KW AIDS; cancer; rheumatoid arthritis; ARDS; cystic fibrosis;
KW tuberculosis; TB; Crohn's disease; sarcoidosis; leprosy; syphilis;
KW malaria; adult respiratory distress syndrome.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "this residue is optionally N-acylated or
glycosylated"

FT Modified-site 11

FT /note= "this residue is optionally in amide or
ester form and may be glycosylated"

XX AU9344664-A.

XX 02-MAR-1995.

XX 12-MAR-1991; 91AU-0074762.

XX 12-MAR-1991; 91AU-0074762.

XX 13-AUG-1993; 93AU-0044664.

XX (PEPT-) PEPTIDE TECHNOLOGY LTD.

XX Ferrante A, Rathjen DA, Widmer F;

XX

DR WPI; 1995-115742/16.
XX Novel peptides which stimulate neutrophils - are fragments of
PT tumour necrosis factor
XX
XX Claim 3; Page 32; 51pp; English.

XX New peptides are provided which prime neutrophils for superoxide
CC production and an enhanced respiratory burst following treatment
CC with N-formyl-L-methionine-L-leucyl-L-phenylalanine. The peptides are
CC described generically. They are fragments from the region of amino acids
CC 54 to 94 of human TNF, or analogues of such fragments. Their
CC neutrophil-stimulating activity can be used in the treatment of diseases
CC such as AIDS, cancer, rheumatoid arthritis, ARDS, cystic fibrosis,
CC tuberculosis, Crohn's disease, sarcoidosis, leprosy, syphilis and
CC malaria. The present sequence is one of 6 specific peptides having the
CC above activity and which fit the the generic formula.

XX Sequence 11 AA;

Query Match 43.3%; Score 26; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHTI 6
Db | | | |
7 ltht1 11

RESULT 8
AAR87684
ID AAR87684 standard; peptide; 11 AA.

AC AAR87684;

DT 10-MAY-1996 (first entry)

DE h-TNF (70-80) analogue.

XX TNF; tumour necrosis factor; neutrophil; superoxide; inflammation;
KW AIDS; cancer; rheumatoid arthritis; ARDS; cystic fibrosis;
KW tuberculosis; TB; Crohn's disease; sarcoidosis; leprosy; syphilis;
KW malaria; adult respiratory distress syndrome.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "this residue is optionally N-acylated or
glycosylated"

FT Modified-site 11

FT /note= "this residue is optionally in amide or
ester form and may be glycosylated"

XX AU9344664-A.

XX 02-MAR-1995.

XX 12-MAR-1991; 91AU-0074762.

XX 12-MAR-1991; 91AU-0074762.

XX 13-AUG-1993; 93AU-0044664.

XX (PEPT-) PEPTIDE TECHNOLOGY LTD.

XX Ferrante A, Rathjen DA, Widmer F;

XX WPI; 1995-115742/16.

XX Novel peptides which stimulate neutrophils - are fragments of
PT tumour necrosis factor

XX

PS Claim 5; Page 32; 51pp; English.

CC New peptides are provided which prime neutrophils for superoxide
CC production and an enhanced respiratory burst following treatment
CC with N-formyl-L-methionine-L-leucyl-L-phenylalanine. The peptides are
CC described generically. They are fragments from the region of amino acids
CC 54 to 94 of human TNF, or analogues of such fragments. Their
CC neutrophil-stimulating activity can be used in the treatment of diseases
CC such as AIDS, cancer, rheumatoid arthritis, ARDS, cystic fibrosis,
CC tuberculosis, Crohn's disease, sarcoidosis, leprosy, syphilis and
CC malaria. The present sequence is one of 6 specific peptides having the
CC above activity and which fit the generic formula.

XX Sequence 11 AA;

SO Query Match 43.3%; Score 26; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
Db 7 lthti 11

RESULT 9
AA52581
ID AAY52581 standard; peptide; 11 AA.
AC AAY52581;
DT 28-FEB-2000 (first entry)
XX
DE Amaranthus viridis amaranthin-1 N-terminal 11-mer peptide.
KW Amaranthin; N-glycosidase; ribosome; inactivation; antiviral;
KW inactivation; protein synthesis; N-glycosidase; adenine; ribosomal RNA;
KW elongation factor 2; EF2-dependent GTPase; irreversible; inhibition;
KW infectivity; reduction; replication; plant virus; tobacco mosaic virus;
KW watermelon mosaic virus; cauliflower mosaic virus; potato virus X;
KW potato virus Y; potato leafroll virus; cucumber mosaic virus;
KW human disease; HIV-1; recombinant expression.
XX
OS Synthetic.
OS Amaranthus viridis.
XX
XX US6001986-A.
XX
PD 14-DEC-1999.
XX
PF 22-AUG-1997; 97US-0916443.
XX
PR 22-AUG-1997; 97US-0916443.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
XX Kim YS, Cho JW, Chung CH, Park SC, Oh SK, Lee H;
XX WPI; 2000-061906/05.
XX
XX Isolated DNA encoding antiviral proteins amaranthin 1 and 2, from
PT Amaranthus viridis.
XX
XX Claim 5; Column 3; 19pp; English.

CC This sequence represents the N-terminal 11 residues of amaranthin-1, an
CC antiviral protein from Amaranthus viridis. Amaranthin-1 (AAV52586) and
CC amaranthin-2 (AAV52587) are inactivators of eukaryotic ribosomes. They
CC have N-glycosidase activity, cleaving the N-glycosidic bond of
CC adenine in a specific ribosomal RNA sequence, thus modifying
CC the EF (elongation factor)-2-dependent GTPase activity of
CC the ribosomal subunit. This irreversibly impairs protein
CC synthesis. Amaranthins 1 and 2 have been shown to reduce infectivity of

CC tobacco mosaic virus and other plant viruses including watermelon
CC mosaic virus, cauliflower mosaic virus, potato virus X and Y, potato
CC leafroll virus and cucumber mosaic virus. These proteins may also be
CC very important to inhibit replication by human viruses, e.g., HIV-1.
CC DNA encoding amaranthins 1 and 2 may be used in expression vectors for
CC the recombinant expression of these antiviral proteins in a host cell.

XX Sequence 11 AA;

SO Query Match 43.3%; Score 26; DB 21; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTHITK 8
Db 3 lthvtk 9

RESULT 10
AAW35497
ID AAW35497 standard; peptide; 12 AA.
AC AAW35497;
XX
XX 22-APR-1998 (first entry)
XX
DE TNF alpha peptide from WO9738011.
XX
KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KW scaffold; inhibition; metastasis; wound healing; solid phase.
XX
OS Unidentified.
XX
XX WO9738011-A1.
XX
PD 16-OCT-1997.
XX
PF 03-APR-1997; 97WO-DE00146.
XX
PR 03-APR-1996; 96DK-0000398.
XX
XX (PEPR-) PEPRESEARCH AS.
XX
XX Heegaard PMH, Jakobsen PH;
XX WPI; 1997-512645/47.
XX
XX Non-dendritic peptide carrier linked to a solid phase - useful as a
XX diagnostic agent and as a scaffold for production of chemical
XX derivatives

XX Example 7; Page 99; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary, and
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence
CC represents a peptide used in an example from the present invention. An
CC (A)-solid phase complex can be used as a scaffold for the production of
CC chemical derivatives, characterised by covalently attaching molecules at
CC attachment points. Alternatively (A) is used as a scaffold-peptide for
CC the incorporation into an Immunostimulating Complex (Iscom) resulting in
CC (A)-Iscom complex which is used for the chemical coupling of antigenic
CC substances in an aqueous solution by conjugation. (A) derivatised with
CC one or more peptides having fibronectin-, laminin- or vitronectin-like
CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules

CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease.

SQ Sequence 12 AA;

Query Match 43.3%; Score 26; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
 |||||
Db 8 lthti 12

RESULT 11
AAY46762
ID AAY46762 standard; Peptide: 9 AA.

XX AC AAY46762;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1373.

XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.

XX OS Synthetic.
OS Homo sapiens.

XX PN WO9945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX PS WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -

XX PS Claim 1; Page 84; 150pp; English.

XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.

XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)

XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful

CC therapeutically and for immunisation as above.

XX SQ Sequence 9 AA;

Query Match 41.7%; Score 25; DB 20; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLTHITIK 8
 :| | :||
Db 2 slvhnltk 9

RESULT 12

AAG89420
ID AAG89420 standard; Peptide: 8 AA.

XX AC AAG89420;

XX DT 11-SEP-2001 (first entry)

XX DE p53 DR supermotif binding peptide core sequence #36.

XX KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
KW vaccine; epitope; cytostatic.

XX OS Homo sapiens.
OS Synthetic.

XX PN WO200141788-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US33629.

XX PR 10-DEC-1999; 99US-0458297.

XX PA (EPIM-) EPIMUNE INC.

XX PI Flakes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX PI Keogh E;

XX PS WPI; 2001-381493/40.

XX PT Epitope-based vaccines comprising p53 epitope having a specified
XX sequences, useful for treating and preventing cancer, the epitopic
XX peptides is useful as diagnostic agents and for evaluating immune
XX response -

XX PS Disclosure; Page 111; 138pp; English.

XX CC The present invention describes isolated prepared p53 epitopes (I). Also
XX described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
XX in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
XX and a second epitope and has less than 50 contiguous amino acids; (3) a
XX vaccine composition comprising (II), a unit dose of a peptide with less
XX than 50 contiguous amino acids with 100% identity to the native peptide
XX sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
XX acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
XX has cytostatic activity and can be used in vaccines. The vaccine
XX composition is useful for treating or preventing cancer. (I) and (II)
XX are useful as diagnostic agents and for evaluating immune responses.
XX Unlike conventional epitopes, immunosuppressive epitopes that may be
XX present in whole antigens can be avoided with the use of the vaccine
XX composition of (I). The ability to combine selected epitopes and
XX further, to modify the composition of the epitopes enhances the
XX immunogenicity. The possible pathological side effects caused by
XX infectious agents or whole protein antigens, which might have their own
XX intrinsic biological activity, are eliminated. AAG89363 to AAG89747
XX represent amino acid sequences used in the exemplification of the
XX present invention.

```
XX SQ Sequence 8 AA;
Query Match 40.0%; Score 24; DB 22; Length 8;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LTHTI 6
Db 1 lthtl 5

RESULT 13
AAG89421
ID AAG89421 standard; Peptide; 8 AA.
XX AC AAG89421;
XX DT 11-SEP-2001 (first entry)
XX DE p53 DR supermotif binding peptide core sequence #37.
XX KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
KW vaccine; epitope; cytostatic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200141788-A1.
XX PN 14-JUN-2001.
XX PF 11-DEC-2000; 2000WO-US33629.
XX PR 10-DEC-1999; 99US-0458297.
XX PR (EPIM-) EPIMUNE INC.
XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
XX PI Keogh E;
XX WPI; 2001-381493/40.
XX Epitope-based vaccines comprising p53 epitope having a specified
XX sequences, useful for treating and preventing cancer, the epitopic
XX peptides is useful as diagnostic agents and for evaluating immune
XX response -
XX Disclosure; Page 111; 138pp; English.
XX The present invention describes isolated prepared p53 epitopes (I). Also
XX described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
XX in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
XX and a second epitope and has less than 50 contiguous amino acids; (3) a
XX vaccine composition comprising (II), a unit dose of a peptide with less
XX than 50 contiguous amino acids with 100% identity to the native peptide
XX sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
XX acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
XX has cytostatic activity and can be used in vaccines. The vaccine
XX composition is useful for treating or preventing cancer. (I) and (II)
XX are useful as diagnostic agents and for evaluating immune responses.
XX Unlike conventional epitopes, immunosuppressive epitopes that may be
XX present in whole antigens can be avoided with the use of the vaccine
XX composition of (I). The ability to combine selected epitopes and
XX further, to modify the composition of the epitopes enhances the
XX immunogenicity. The possible pathological side effects caused by
XX infectious agents or whole protein antigens, which might have their own
XX intrinsic biological activity, are eliminated. AAG89363 to AAG89747
XX represent amino acid sequences used in the exemplification of the
XX present invention.

SQ Sequence 8 AA;
Query Match 40.0%; Score 24; DB 22; Length 8;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LTHTI 6
Db 1 lthtl 5

RESULT 14
AAW30080
ID AAW30080 standard; Peptide; 10 AA.
XX AC AAW30080;
XX DT 27-MAR-1998 (first entry)
XX DE Hamster neuritin internal peptide P3.
XX KW Neuritin; glial-derived neurotrophic factor; GDNF; persephin;
KW hamster.
XX OS Cricetulus sp.
XX PN WO9733911-A1.
XX PN 18-SEP-1997.
XX PF 14-MAR-1997; 97WO-US03461.
XX PR 14-MAR-1996; 96US-0615944.
XX PR (UNIW ) UNIV WASHINGTON.
XX PA Johnson EM, Kotzbauer PT, Lampe PA, Milbrandt JD;
XX WPI; 1997-470818/43.
XX GDNF-neurturin family related growth factor, Persephin - used to
XX prevent or treat cellular, neuronal or non-neuronal, degeneration or
XX insufficiency
XX Example 4; Page 125; 228pp; English.
XX This peptide sequence comprises internal peptide P3 of hamster
XX neuritin isolated from CHO cell conditioned medium. Other
XX internal peptides (see AAW30078-79) and an N-terminal peptide (see
XX AAW30077) of hamster neuritin have also been isolated. Probes and
XX primers based on these peptide sequences and used to obtain
XX neuritin cDNA clones from related species; PCR primers (see
XX AAW90764-65) based on internal peptides P2 and P3 were used to
XX isolate mouse and human neuritin cDNA clones. Neuritin is a
XX member of the glial-derived neurotrophic factor (GDNF) family.
XX A novel member of the GDNF-neurturin growth factor family,
XX persephin (see AAW30064-68), was subsequently identified that can
XX be used in claimed methods for preventing or treating neuronal
XX degeneration, haematopoietic cell degeneration and cardiac muscle
XX degeneration or insufficiency.
XX Sequence 10 AA;
Query Match 40.0%; Score 24; DB 18; Length 10;
Best Local Similarity 50.0%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 HPTIKLNA 11
Db 2 htlqelsa 9
```

RESULT 15
AAW13715
ID AAW13715 standard; Peptide; 10 AA.
XX
AC AAW13715;
XX
DT 09-FEB-1998 (first entry)
XX
DE Internal neurturin fragment P3.
XX
KW Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;
KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;
KW monocytopenia; neutropaenia; anaemia; thrombocytopaenia; neuroblastoma;
KW antibody; obesity; therapy; hamster.
XX
OS Cricetulus griseus.
XX
PN WO9708196-A1.
XX
PD 06-MAR-1997.
XX
PF 27-AUG-1996; 96WO-US14065.
XX
PR 28-AUG-1995; 95US-0519777.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Johnson EM, Kotzbauer PT, Lampe PA, Milbrandt JD;
XX
DR WPI; 1997-179176/16.
XX
PT A novel growth factor Neurturin - used to treat neuro-degenerative
PT and haematopoietic cell degeneration diseases, e.g. Alzheimer's
PT disease and eosinopenia
XX
PS Example 5; Page 8; 206pp; English.
XX
CC AAW13712-W13715 represent internal fragments of neurturin (NT). These
CC sequences, and the N-terminal fragment shown in AAW13712, were isolated
CC from chinese hamster ovary (CHO) cells. These sequences were used to
CC produce degenerate primers (see AAT61481 and AAT61482) which were used
CC to isolate the human and mouse NT coding sequences (see AAT61468 and
CC AAT61469 respectively). NT promotes the growth and differentiation of
CC haematopoietic and neuronal cells, and their stem cells. The NT gene and
CC protein are used to prevent or treat neurodegenerative diseases e.g.
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, ischaemic stroke,
CC acute brain injury, acute spinal cord injury, nervous system tumours,
CC multiple sclerosis and infection; and haematopoietic cell degenerative
CC diseases, e.g. eosinopenia, basopaenia, lymphopaenia, monocytopenia,
CC neutropaenia, anaemia, thrombocytopaenia and stem cell insufficiencies.
CC The NT protein and gene are also useful to treat neuroblastomas.
CC Antibodies against NT and oligonucleotides (used as either probes or
CC primers, corresponding to an exon of pre-pro-NT gene or flanking a
CC target sequence) can be used for detecting NT in a sample or detecting
CC mutations in the NT gene. Antisense sequences of the NT gene are used to
CC treat diseases promoted by NT expression e.g. obesity.
XX
SQ Sequence 10 AA;

Query Match 40.08; Score 24; DB 18; Length 10;
Best Local Similarity 50.08; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 HTITKLN 11
||: :|:|
Db 2 htiqlsa 9

RESULT 16
AAY16636
ID AAY16636 standard; Peptide; 10 AA.
XX
AC AAY16636;
XX
DT 17-AUG-1999 (first entry)
XX
DE WO9914235 Seq ID No: 6.
XX
KW Growth factor; GF; persephin; neuron growth; cellular degeneration;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischaemic stroke;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
KW brain injury; spinal cord injury; nervous system tumour; infection;
KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;
KW metabolic disease; diabetes; renal dysfunction; neurturin.
XX
OS Mus sp.
XX
PN WO9914235-A1.
XX
PD 25-MAR-1999.
XX
PF 15-SEP-1998; 98WO-US19163.
XX
PR 16-SEP-1997; 97US-0931858.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Desauvage F, Johnson EM, Klein R, Kotzbauer PT;
PI Lampe PA, Milbrandt JD;
XX
DR WPI; 1999-244023/20.
XX
PT New isolated persephin growth factor nucleic acids used to, e.g.
PT promote neuronal growth
XX
PS Example 5; Page 125; 222pp; English.
XX
CC The invention relates to a novel isolated and purified growth factor (GF)
CC that comprises persephin or a fragment or a conservatively substituted
CC variant. The persephin GF polypeptides can promote the survival and
CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
CC or polynucleotides can be used for preventing or treating cellular
CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, ischaemic stroke,
CC acute brain injury, acute spinal cord injury, nervous system tumours,
CC multiple sclerosis, or infection, hematopoietic cell degeneration or
CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
CC resulting from cardiomyopathy or congestive heart failure. They can also
CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
CC and damage caused by infectious agents. The GF can also be used for
CC promoting the growth and/or differentiation of a cell in a culture
CC medium. The antisense polynucleotides can be used for treating a disease
CC condition mediated by expression of persephin by a population of cells.
CC The products can also be used for detection and diagnosis.
XX
SQ Sequence 10 AA;

Query Match 40.08; Score 24; DB 20; Length 10;
Best Local Similarity 50.08; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 HTITKLN 11
||: :|:|
Db 2 htiqlsa 9

```

RESULT 17
AAM42846
ID AAM42846 standard; Peptide; 10 AA.
AC AAM42846;
XX
XX 22-OCT-2001 (first entry)
DT
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 155.
XX
XX Mycoplasma genitalium; complementary peptide; ligand;
KW protein-protein interaction; drug design; intermolecular;
XX intramolecular.
XX
XX Mycoplasma genitalium.
OS
XX WO200142278-A2.
PN
XX 14-JUN-2001.
PD
XX 13-DEC-2000; 2000WO-GB04778.
PF
XX 13-DEC-1999; 99GB-0029466.
PR
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
PI
XX WPI; 2001-514238/56.
DR
XX
XX Complementary peptide ligands as reagents and drugs for drug discovery
PT programs and as lead ligands to facilitate drug design and development,
PT are generated from microbial genome sequences -
XX
XX Example 2; Page 71; 161pp; English.
XX
XX The present sequence is one of a large number of complementary peptide
CC ligands generated from Mycoplasma genitalium genome sequences. These
CC specific complementary peptides interact with their relevant target
CC proteins encoded by the microbial genome. They are capable of
CC antagonising or agonising specific interaction of a protein with
CC another protein or receptor and are thus useful as reagents and drugs,
CC and as lead ligands to facilitate drug design and development. They
CC are useful as tools for functional genomic studies, reagents for the
CC configuration of high-throughput screens, as a starting point for
CC medicinal chemistry manipulation, for peptide mimetics and as
CC therapeutic agents. The analysis and acquisition of peptide sequences
CC facilitates understanding of protein-protein interactions. The method
CC allows for analysis of an entire database at a time, thus overcoming
CC sampling problems. The set of complementary peptides includes both
CC intermolecular (between proteins) and intermolecular (within a
CC protein) sequences.
XX
XX Sequence 10 AA;

Query Match 40.0%; Score 24; DB 22; Length 10;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TITKLN 10
DB 2 tinkln 7

RESULT 18
AAR87683
ID AAR87683 standard; peptide; 11 AA.
XX
XX AAR87683;
XX
XX 10-MAY-1996 (first entry)
DT

h-TNF (70-80) analogue.
XX
XX TNF; tumour necrosis factor; neutrophil; superoxide; inflammation;
KW AIDS; cancer; rheumatoid arthritis; ARDS; cystic fibrosis;
KW tuberculosis; TB; Crohn's disease; sarcoidosis; leprosy; syphilis;
KW malaria; adult respiratory distress syndrome.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "this residue is optionally N-acetylated or
FT glycosylated"
FT Modified-site 11 /note= "this residue is optionally in amide or
FT ester form and may be glycosylated"
XX
XX AU9344664-A.
PN
XX 02-MAR-1995.
PD
XX 12-MAR-1991; 91AU-0074762.
PF
XX 12-MAR-1991; 91AU-0074762.
PR 13-AUG-1993; 93AU-0044664.
XX
XX (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX
XX Ferrante A, Rathjen DA, Widmer F;
PI
XX WPI; 1995-115742/16.
DR
XX
XX Novel peptides which stimulate neutrophils - are fragments of
PT tumour necrosis factor
PT
XX
XX Claim 4; Page 32; 51pp; English.
XX
XX New peptides are provided which prime neutrophils for superoxide
CC production and an enhanced respiratory burst following treatment
CC with N-formyl-L-methionine-L-leucyl-L-phenylalanine. The peptides are
CC described generically. They are fragments from the region of amino acids
CC 54 to 94 of human TNF, or analogues of such fragments. Their
CC neutrophil-stimulating activity can be used in the treatment of diseases
CC such as AIDS, cancer, rheumatoid arthritis, ARDS, cystic fibrosis,
CC tuberculosis, Crohn's disease, sarcoidosis, leprosy, syphilis and
CC malaria. The present sequence is one of 6 specific peptides having the
CC above activity and which fit the the generic formula.
XX
XX Sequence 11 AA;

Query Match 40.0%; Score 24; DB 16; Length 11;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHITI 6
DB 7 ithiti 11

RESULT 19
AAW35449
ID AAW35449 standard; peptide; 11 AA.
XX
XX AAW35449;
AC
XX
XX 22-APR-1998 (first entry)
DT
XX
XX Cytokine derived peptide from TNF (70-80).
DE
XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KW scaffold; inhibition; metastasis; wound healing; solid phase.

```

XX OS Unidentified.
XX PN WO9738011-A1.
XX PD 16-OCT-1997.
XX PF 03-APR-1997; 97WO-DE00146.
XX PR 03-APR-1996; 96DK-0000398.
XX PA (PEPR-) PEPRSEARCH AS.
XX PI Heegaard PMH, Jakobsen PH;
XX WPI; 1997-512645/47.
XX DR
XX PT Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives
XX PS Claim 30; Page 199; 262pp; English.
XX CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence
CC represents a specifically claimed cytokine derived peptide from the
CC present invention. An (A)-solid phase complex can be used as a scaffold
CC for the production of chemical derivatives, characterised by covalently
CC attaching molecules at attachment points. Alternatively (A) is used as
CC a scaffold-peptide for the incorporation into an immunostimulating
CC complex (Iscom) resulting in an (A)-Iscom complex which is used for the
CC chemical coupling of antigenic substances in an aqueous solution by
CC conjugation. (A) derivatised with one or more peptides having
CC fibronectin-, laminin- or vitronectin-like binding activities can be
CC used for the promotion of cell-attachment to plastic surfaces, in
CC particular to inhibit tumour growth and metastasis, and for promotion
CC of wound healing. Also a derivatised (A) can be used for the selection
CC of specifically-binding aptamers or as a diagnostic agent. Such
CC diagnostic-(A) molecules could be used to detect molecules derived from
CC or indicative of pregnancy or of a disease, such as an infectious,
XX autoimmune or cancerous disease.
XX SQ Sequence 11 AA;

Query Match 40.0%; Score 24; DB 18; Length 11;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LTHTI 6
Db :||||
7 ithti 11

RESULT 20
AAW47911
ID AAW47911 standard; peptide; 11 AA.
XX AC AAW47911;
XX XX
XX DT 09-JUN-1998 (first entry)
XX DE Human tumour necrosis factor derived peptide 1168.
XX KW Human; tumour necrosis factor; neutrophil; monocyte; macrophage;
XX KW stimulatory activity; immunosuppressant; cancer; infection.
XX OS Synthetic.
OS Homo sapiens.

XX WO9748725-A1.
XX PN
XX PD 24-DEC-1997.
XX PF 20-JUN-1997; 97WO-AU00395.
XX PR 29-OCT-1996; 96AU-0003309.
XX PR 21-JUN-1996; 96AU-0000610.
XX PR 06-SEP-1996; 96AU-0002165.
XX PA (PEPT-) PEPTTECH LTD.
XX PI Mack PO, Rathjen DA, Sleight JM, Widmer F;
XX WPI; 1998-063077/06.
XX DR
XX PT Tumour necrosis factor derived peptide(s) having neutrophil and/or
PT monocyte-macrophage stimulatory activity - used for treating e.g.
PT infections, immunosuppression or cancers
XX PS Claim 4; Page 44; 65pp; English.
XX CC The present sequence represents a peptide derived from a human tumour
CC necrosis factor peptide. The peptide can have neutrophil and/or
CC monocyte/macrophage stimulatory activity. The peptide is derived from
CC the sequence of tumour necrosis factor (TNF)-derived peptide 419
CC (PSTHVLTHHT; see AU74762/91 and 44664/93). It can have improved
CC properties such as increased potency, extended in vivo half life or,
CC particularly, specificity of action. It can have neutrophil stimulatory
CC activity (class 1), equal neutrophil and monocyte/macrophage stimulatory
CC activity (class 2), or preferentially enhanced monocyte/macrophage
CC stimulatory activity (class 3). It can be used for the treatment or
CC prevention of infections. In particular, it can be used for treating
CC AIDS, cancer, diabetes, nosocomial infection, tuberculosis, cystic
CC fibrosis, community acquired pneumonia, meningitis, Mycobacterias,
CC Chlamydia, Brucellae, Francisella, Pasteurellosis, Legionellosis,
CC Histoplasmosis, Listeriosis, Pneumocystis carinii, Trypanosoma cruzi,
CC coccidian parasitic infection, an inherited primary neutropenic
CC disorder, an inherited primary defect of phagocytic cell function, an
CC inherited secondary defect of phagocytic cell function, an acquired
CC defect of phagocytic cell function, immunosuppression due to the
CC administration of immunosuppressive drugs, and other bacterial, fungal,
CC viral or protozoan infection, infectious mononucleosis, paroxysmal
CC nocturnal, haemoglobinuria, leukaemia, lymphoma, myelofibrosis, or graft
CC versus host disease.
XX SQ Sequence 11 AA;

Query Match 40.0%; Score 24; DB 19; Length 11;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LTHTI 6
Db :||||
7 ithti 11

Search completed: July 8, 2002, 11:42:57
Job time: 229 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:40:58 ; Search time 21.49 Seconds
(without alignments)
13.639 Million cell updates/sec

Title: US-09-461-061A-2
Perfect score: 60
Sequence: 1 TLTHITIKLNAE 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 83765

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	51.7	9	1	US-08-107-235-13
2	31	51.7	9	3	US-08-714-960B-13
3	26	43.3	9	1	US-08-259-550A-21
4	26	43.3	10	4	US-09-177-249-131
5	26	43.3	11	1	US-08-107-235-15
6	26	43.3	11	1	US-08-107-235-17
7	26	43.3	11	3	US-08-916-443A-1
8	26	43.3	11	3	US-08-714-960B-15
9	26	43.3	11	3	US-08-714-960B-17
10	24	40.0	10	1	US-08-519-777-6
11	24	40.0	10	1	US-08-742-035-6
12	24	40.0	10	2	US-08-777-019-6
13	24	40.0	10	2	US-08-777-143-6
14	24	40.0	10	3	US-08-775-414-6
15	24	40.0	10	4	US-08-931-858E-6
16	24	40.0	10	4	US-08-981-739-6
17	24	40.0	11	1	US-08-107-235-18
18	24	40.0	11	3	US-08-714-960B-18
19	23	38.3	10	2	US-08-025-321C-1
20	23	38.3	12	4	US-09-461-697-138
21	22	36.7	5	4	US-08-751-344B-29
22	22	36.7	7	4	US-08-640-737-38
23	22	36.7	11	4	US-09-306-756-3
24	22	36.7	12	3	US-09-188-579-33
25	22	36.7	12	4	US-09-315-444-33
26	22	36.7	12	4	US-09-268-347-17
27	22	36.7	12	4	US-09-382-689A-6

28 22 36.7 12 4 US-09-261-182-9 Sequence 9, Appl
29 21 35.0 9 4 US-09-258-754-146 Sequence 146, App
30 21 35.0 9 4 US-09-042-107-146 Sequence 146, App
31 21 35.0 11 1 US-07-657-769B-43 Sequence 43, Appl
32 21 35.0 11 1 US-07-789-184-104 Sequence 104, App
33 21 35.0 11 1 US-07-789-184-215 Sequence 215, App
34 21 35.0 11 1 US-07-789-184-218 Sequence 218, App
35 21 35.0 11 1 US-08-475-263-104 Sequence 104, App
36 21 35.0 11 1 US-08-475-263-215 Sequence 215, App
37 21 35.0 11 1 US-08-475-263-218 Sequence 218, App
38 21 35.0 11 1 US-08-485-886-104 Sequence 104, App
39 21 35.0 11 1 US-08-485-886-215 Sequence 215, App
40 21 35.0 11 1 US-08-485-886-218 Sequence 218, App
41 21 35.0 11 2 US-08-477-362-104 Sequence 104, App
42 21 35.0 11 2 US-08-477-362-215 Sequence 215, App
43 21 35.0 11 2 US-08-477-362-218 Sequence 218, App
44 21 35.0 11 2 US-08-477-134-104 Sequence 104, App
45 21 35.0 11 2 US-08-477-134-215 Sequence 215, App

ALIGNMENTS

RESULT 1
US-08-107-235-13
; Sequence 13, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,622A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /note= "PEPTIDE 393 (76-84)"
US-08-107-235-13

Query Match 51.7%; Score 31; DB 1; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.7e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHITTKL 9
Db 1 LHTTISRI 8

RESULT 2
US-08-714-960B-13
; Sequence 13, Application US/08714960B
; Patent No. 6121237
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,960B
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ9065
; FILING DATE: 12-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /note= "PEPTIDE 393 (76-84)"
US-08-714-960B-13

Query Match 51.7%; Score 31; DB 3; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHITTKL 9
Db 1 LHTTISRI 8

RESULT 3
US-08-259-550A-21
; Sequence 21, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-259-550A-21

Query Match 43.3%; Score 26; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHIT 6
Db 5 LHTTI 9

RESULT 4
US-09-177-249-131
; Sequence 131, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-08612005
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22

EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 131
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-131

Query Match 43.3%; Score 26; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HTITKNAE 12
||: |||
DB 1 HTLFKNLE 9

RESULT 5
US-08-107-235-15
; Sequence 15, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,235
FILING DATE: 16-AUG-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 395 (70-80)"

Query Match 43.3%; Score 26; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHTI 6
||||
DB 7 LTHTI 11

RESULT 6
US-08-107-235-17
; Sequence 17, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,235
FILING DATE: 16-AUG-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 418"

US-08-107-235-17
Query Match 43.3%; Score 26; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTHTI 6
||||
DB 7 LTHTI 11

RESULT 7
US-08-916-443A-1
; Sequence 1, Application US/08916443A
; Patent No. 6001986
; GENERAL INFORMATION:
; APPLICANT: Yong Sig KIM
; APPLICANT: Sun Chung PARK
; APPLICANT: Soo Kyung OH
; APPLICANT: Hosull LEE
; APPLICANT: Jeong Woo CHO

APPLICANT: Chang H. CHUNG
TITLE OF INVENTION: Antiviral Proteins, Amarandin 1 and 2, from
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,443A
FILING DATE: 22 AUG 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 1942/18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-443A-1

Query Match 43.3%; Score 26; DB 3; Length 11;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTHVTK 8
Db 3 LTFVTK 9

RESULT 8
US-08-714-960B-15
Sequence 15, Application US/08714960B
Patent No. 612137
GENERAL INFORMATION:
APPLICANT: RATHJEN, Deborah A
APPLICANT: FERRANTE, Antonio
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,960B
FILING DATE: 17-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065

FILING DATE: 12-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 92,622-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 395 (70-80)"
US-08-714-960B-15
Query Match 43.3%; Score 26; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LTHV 6
Db 7 LTHV 11
RESULT 9
US-08-714-960B-17
Sequence 17, Application US/08714960B
Patent No. 612137
GENERAL INFORMATION:
APPLICANT: RATHJEN, Deborah A
APPLICANT: FERRANTE, Antonio
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,960B
FILING DATE: 17-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415

```
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-11
; OTHER INFORMATION: /note= "PEPTIDE 418"
US-08-714-960B-17

Query Match 43.3%; Score 26; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
Db 7 LTHTI 11

RESULT 10
US-08-519-777-6
; Sequence 6, Application US/08519777
; Patent No. 5739307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,777
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-742-035-6

Query Match 40.0%; Score 24; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLA 11
Db 2 HTLQELSA 9

RESULT 12
US-08-777-019-6
; Sequence 6, Application US/08777019
; Patent No. 5817622
; GENERAL INFORMATION:
```

```
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-11
; OTHER INFORMATION: /note= "PEPTIDE 418"
US-08-714-960B-17

Query Match 43.3%; Score 26; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
Db 7 LTHTI 11

RESULT 10
US-08-519-777-6
; Sequence 6, Application US/08519777
; Patent No. 5739307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,777
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-742-035-6

Query Match 40.0%; Score 24; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLA 11
Db 2 HTLQELSA 9

RESULT 12
US-08-777-019-6
; Sequence 6, Application US/08777019
; Patent No. 5817622
; GENERAL INFORMATION:
```

APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,019
FILING DATE: 30-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/519,777
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 953095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-777-019-6

Query Match 40.08; Score 24; DB 2; Length 10;
Best Local Similarity 50.08; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLN 11
||: :||
Db 2 HTLQELSA 9

RESULT 13
US-08-777-143-6
Sequence 6, Application US/08777143
Patent No. 5843914
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,143
FILING DATE: 30-DEC-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/519,777
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 953095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-777-143-6

Query Match 40.08; Score 24; DB 2; Length 10;
Best Local Similarity 50.08; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLN 11
||: :||
Db 2 HTLQELSA 9

RESULT 14
US-08-775-414-6
Sequence 6, Application US/08775414
Patent No. 6090778
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,414
FILING DATE: 31-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965805
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-775-414-6

Query Match 40.0%; Score 24; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLNA 11
||: ||:|
Db 2 HTLQELSA 9

RESULT 15
US-08-931-858E-6
; Sequence 6, Application US/08931858E
; Patent No. 6222022
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M
; APPLICANT: MILBRANDT, JEFFREY D
; APPLICANT: KOTZBAUER, PAUL T
; APPLICANT: LAMPE, PATRICIA A
; APPLICANT: KLEIN, ROBERT
; APPLICANT: DESAUVAGE, FRED
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/931,858E
; APPLICATION NUMBER: US/08/931,858E
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971486
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-931-858E-6

Query Match 40.0%; Score 24; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLNA 11
||: ||:|
Db 2 HTLQELSA 9

RESULT 16
US-08-981-739-6
; Sequence 6, Application US/08981739
; Patent No. 6232449
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.

; KOTZBAUER, PAUL T.
; LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/981,739
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-981-739-6

Query Match 40.0%; Score 24; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HTITKLNA 11
||: ||:|
Db 2 HTLQELSA 9

RESULT 17
US-08-107-235-18
; Sequence 18, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,235
FILING DATE: 16-AUG-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 419"
US-08-107-235-18

Query Match 40.0%; Score 24; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
:||||
Db 7 ITHTI 11

RESULT 18
US-08-714-960B-18
Sequence 18, Application US/08714960B
Patent No. 6121237
GENERAL INFORMATION:
APPLICANT: RATHJEN, Deborah A
APPLICANT: FERRANTE, Antonio
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: Wordperfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,960B
FILING DATE: 17-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 92,622-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 419"
US-08-714-960B-18

Query Match 40.0%; Score 24; DB 3; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTHTI 6
:||||
Db 7 ITHTI 11

RESULT 19
US-08-025-321C-1
Sequence 1, Application US/08025321C
Patent No. 5849560
GENERAL INFORMATION:
APPLICANT: Abraham Ph.D., Carmela R.
TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGRADATION
OF AMYLOID BETA-PROTEIN PRECURSOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/025,321C
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0079571-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 248 5000
TELEFAX: 617 248 4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-025-321C-1

Query Match 38.3%; Score 23; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 HTITKLNAE 12
I: |||
Db 1 HSEVKMDAE 9

RESULT 20
US-09-461-697-138
; Sequence 138, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-138

Query Match 38.3%; Score 23; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. NO. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TKLNAE 12
I: |||
Db 7 TKLNNE 12

Search completed: July 8, 2002, 11:43:26
Job time: 148 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:43:57 ; Search time 24.98 seconds
(without alignments)
46.160 Million cell updates/sec

Title: US-09-461-061a-3

Perfect score: 56

Sequence: 1 IDNVKKARVQVV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1579

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	41.1	10	2 PS0220	ferredoxin--NADP+
2	22	39.3	10	2 S70251	nitrogenase (EC 1.1.8.1)
3	20	35.7	11	2 S33519	probable secreted
4	20	35.7	12	2 E64573	hypothetical prote
5	19	33.9	12	2 D28551	hypothetical prote
6	18	32.1	10	2 PA0116	ferredoxin--NADP+
7	17	30.4	7	2 A28709	phosphonocataldehy
8	17	30.4	11	2 JQ0395	hypothetical prote
9	16	28.6	10	2 S70722	65.4K GTP-binding
10	16	28.6	11	2 S19301	endo-1,4-beta-xyla
11	15	26.8	17	2 A15398	choline oxidase (E
12	15	26.8	10	2 PC2044	beta-kirilowin - M
13	15	26.8	11	2 S21727	gamma-interferon-i
14	15	26.8	12	2 A60757	enterotoxin C-1 -
15	15	26.8	12	2 S18722	matK protein - bee
16	15	26.8	12	2 S65626	phosphorylase b -
17	14	25.0	6	2 B50110	repetitive protein
18	14	25.0	7	2 S19630	ribosomal protein
19	14	25.0	8	2 T10077	hypothetical prote
20	14	25.0	9	2 PS0253	glycine cleavage s
21	14	25.0	10	2 A32543	cardioexcitatory n
22	14	25.0	10	2 F44644	neurotoxin-associ
23	14	25.0	10	2 PQ0788	NADH dehydrogenase
24	14	25.0	10	2 PS0451	24K protein 4302 -
25	14	25.0	10	2 A42089	transcription fact
26	14	25.0	10	2 A56633	neomycinopressin -
27	14	25.0	10	2 E86128	hypothetical prote
28	14	25.0	11	2 PH1343	Ig heavy chain DJ
29	14	25.0	11	2 PN0044	protein kinase C 1

30 14 25.0 12 2 A39233 myosin heavy chain
31 14 25.0 12 2 S36902 Em protein - wheat
32 14 25.0 12 2 C61308 hemocyanin chain 6
33 14 25.0 12 2 A34858 proteinase E - bla
34 14 25.0 12 2 I77529 estrogen receptor
35 14 25.0 12 2 S21205 Ig heavy chain V r
36 14 25.0 12 2 I46922 gene Bata protein
37 13 23.2 6 2 PC4392 whey glycoprotein
38 13 23.2 7 2 A34818 vicilin 72K chain
39 13 23.2 8 2 A39892 P element, P cytot
40 13 23.2 8 2 S66296 Na+-transporting A
41 13 23.2 9 2 B39841 dextranucrase (EC
42 13 23.2 9 2 A39841 sucrose 3-glucosyl
43 13 23.2 9 2 S78426 52.5K protein - sp
44 13 23.2 10 2 PC2172 triacylglycerol 11
45 13 23.2 10 2 C38925 seed storage prote

ALIGNMENTS

RESULT 1

PS0220

ferredoxin--NADP+ reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Feb-1997

C:Accession: PS0220

R:Uchiyama, Y.; Tsugita, A.

submitted to JIPID, August 1991

A:Reference number: PS0205

A:Accession: PS0220

A:Molecule type: protein

A:Residues: 1-10 <UCH>

C:Keywords: NADP; oxidoreductase

Query Match 41.1%; Score 23; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 4e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDNVKKARVQ 10

Db 1 VERVSKKQVQ 10

RESULT 2

S70251

nitrogenase (EC 1.18.6.1) iron protein - Anabaena variabilis (fragment)

C:Species: Anabaena variabilis

C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 19-Jan-2001

C:Accession: S70251

R:Schrautemeier, B.; Neveling, U.; Schmitz, S.

Mol. Microbiol. 18, 357-369, 1995

A>Title: Distinct and differently regulated Mo-dependent nitrogen-fixing systems evol
regions as part of the nifH/2 gene clusters.

A:Reference number: S70251

A:Accession: S70251

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-10 <SCH>

A:Cross-references: EMBL:U25160; NID:gl160347; PIDN:AC43540.1; PID:gl160348

A:Experimental source: ATCC 29413

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C:Genetics:

A:Gene: nifH2

C:Keywords: ATP; iron-sulfur protein; nitrogen fixation; oxidoreductase

Query Match 39.3%; Score 22; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 6.1e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDNVKK 6

Db 4 DVPTAAVQ 11
: | | | |

RESULT 14

A60757

enterotoxin C-1 - Staphylococcus aureus (fragments)

C:Species: Staphylococcus aureus

C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 30-Sep-1993

C:Accession: A60757

R:Bohach, G.A.; Handley, J.P.; Schlievert, P.M.

Infect. Immun. 57, 23-28, 1989

A:Title: Biological and immunological properties of the carboxyl terminus of staphylococ

A:Reference number: A60757; MUID:89079292

A:Accession: A60757

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BOH>

Query Match

26.8%; Score 15; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVK 5

Db 3 DRVK 6

RESULT 15

S18722

matK protein - beechdrops plastid (fragment)

C:Species: plastid Epifagus virginiana (beechdrops)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Feb-1995

C:Accession: S18722

R:Morden, C.W.; Wolfe, K.H.; dePamphilis, C.W.; Palmer, J.D.

EMBO J. 10, 3281-3288, 1991

A:Title: Plastid translation and transcription genes in a non-photosynthetic plant: inte

A:Reference number: S17794; MUID:92007779

A:Accession: S18722

A:Molecule type: DNA

A:Residues: 1-12 <MOR>

A:Cross-references: EMBL:X61798

C:Genetics:

A:Gene: matK

A:Genome: plastid

C:Keywords: plastid

Query Match

26.8%; Score 15; DB 2; Length 12;

Best Local Similarity 40.0%; Pred. No. 1.5e+04;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDNVK 5

Db 1 MDKIK 5

RESULT 16

S65626

phosphorylase b - rabbit (fragments)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S65626

R:Luo, S.; Martin, B.L.; Senshu, T.; Graves, D.J.

Arch. Biochem. Biophys. 318, 362-369, 1995

A:Title: Enzymatic deamination of glycogen phosphorylase and a peptide of the phosphoryl

A:Reference number: S65626; MUID:95211385

A:Accession: S65626

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-34-12 <LUO>

Query Match 26.8%; Score 15; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNV 4

Db 8 VENV 11

RESULT 17

B60110

repetitive protein antigen 61 - Trypanosoma cruzi (fragment)

C:Species: Trypanosoma cruzi

C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993

C:Accession: B60110

R:Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J

Infect. Immun. 57, 1959-1967, 1989

A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.

A:Reference number: A60110; MUID:89277508

A:Accession: B60110

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-6 <ROF>

A:Note: this is an example of a five residue tandem repeat from this protein; the act

C:Keywords: tandem repeat

Query Match

25.0%; Score 14; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKA 7

Db 4 KKA 6

RESULT 18

S19630

ribosomal protein L30 - Streptomyces griseus (fragment)

C:Species: Streptomyces griseus

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997

C:Accession: S19630

R:Ochi, K.

Int. J. Syst. Bacteriol. 42, 144-150, 1992

A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete

A:Reference number: S19630; MUID:92144363

A:Accession: S19630

A:Molecule type: protein

A:Residues: 1-7 <OCH>

A:Experimental source: strain IFO 13189

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match

25.0%; Score 14; DB 2; Length 7;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARVOV 11

Db 1 ARUKI 5

RESULT 19

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C:Species: Methylophilus methylotrophus

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10077

R:Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.

J. Bacteriol. 176, 4073-4080, 1994

A:Title: Organization of the methylamine utilization (mau) genes in Methylophilus met

A:Reference number: Z16936; MUID:94292427
A:Accession: T10077
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <CHI>
A:Cross-references: EMBL:L26407; NID:G561931; PIDN:AAB46955.1; PID:G561933
A:Experimental source: strain W3A1
C:Genetics:
A:Gene: mauN

Query Match 25.0%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 RVQVV 12
I: I:
Db 3 RLQAI 7

RESULT 20
PS0253
glycine cleavage system protein H - rice (strain Nihonbare) (fragment)
N:Alternate names: glycine decarboxylase complex H protein
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Feb-1994
C:Accession: PS0253
R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0253
A:Molecule type: protein
A:Residues: 1-9 <TSU>

Query Match 25.0%; Score 14; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IDNVK 5
I: I:
Db 4 LDGLK 8

Search completed: July 8, 2002, 11:43:58
Job time: 159 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:48:58 ; Search time 13.1 Seconds
(without alignments)
35.468 Million cell updates/sec

Title: US-09-461-061A-3
Perfect score: 56
Sequence: 1 IDNVKKARQVQV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 463

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query %		Length	DB	ID	Description		
		Match							
1	19	33.9	11	1	ES1_RAT	P56571	rattus norv		
2	17	30.4	12	1	ULAL_MOUSE	P99032	mus musculus		
3	16	28.6	12	1	HCYB_MEGCR	Q10584	megathura c		
4	15	26.8	7	1	CHOX_ALCSP	P16101	alcaligenes		
5	15	26.8	12	1	RS19_TOBBP	Q56251	tomato big		
6	14	25.0	9	1	ULAD_HUMAN	P31929	homo sapien		
7	14	25.0	10	1	FARP_LOCFI	P38553	locusta mig		
8	14	25.0	10	1	LCMS_LEUMA	P21144	leucophaea		
9	14	25.0	10	1	NEMS_DROME	P41494	drosophila		
10	14	25.0	11	1	CSI5_BACSU	P81095	bacillus su		
11	13	23.2	7	1	UH11_RAT	P56576	rattus norv		
12	13	23.2	9	1	IPYR_RHOVI	P82992	rhodopsendo		
13	13	23.2	9	1	RS10_SERMA	O68936	serratia ma		
14	13	23.2	10	1	COXQ_RABIT	P80336	oryctolagus		
15	13	23.2	10	1	UXA6_CHLTR	P38007	chlamydia t		
16	13	23.2	12	1	FAR1_CALVO	P41869	calliphora		
17	13	23.2	12	1	OPS3_DROVI	P17645	drosophila		
18	13	23.2	12	1	RS19_KLYEP	Q46490	clover yell		
19	13	23.2	12	1	UH03_RAT	P56572	rattus norv		
20	12	21.4	7	1	FARB_CALVO	P41866	calliphora		
21	12	21.4	9	1	LPCA_STAAU	P36884	staphylococ		
22	12	21.4	10	1	ANG1_BOVJA	Q10581	bothrops ja		
23	12	21.4	10	1	ANGT_BOVIN	P01017	bos taurus		
24	12	21.4	10	1	ANGT_CHICK	P01018	gallus gall		
25	12	21.4	10	1	COXA_ONCHY	P80328	oncorhynch		
26	12	21.4	10	1	FARC_CALVO	P41867	calliphora		
27	12	21.4	10	1	FIBB_CERSI	P14537	ceratotheri		
28	12	21.4	10	1	MALE_KLEPN	Q05564	klebsiella		
29	12	21.4	10	1	NS1_MYCTU	P81135	mycobacteri		
30	12	21.4	10	1	ODP2_BOVIN	P11180	bos taurus		
31	12	21.4	10	1	RRPL_PHODY	P35946	phocine dis		
32	12	21.4	10	1	TEMK_RANTE	P56923	rana tempor		
33	12	21.4	10	1	UPA9_HUMAN	P30095	homo sapien		

34 12 21.4 11 1 HS70_PINPS P81672 pinus pinas
35 12 21.4 11 1 TRNA_GADMO P28498 gadus morhu
36 12 21.4 12 1 DCML_PSECA P19919 pseudomonas
37 12 21.4 12 1 LICH_BACLI P82907 bacillus li
38 12 21.4 12 1 YZPY_ECOLI P17776 escherichia
39 11 19.6 8 1 ACT_CARMA P80709 carcinus ma
40 11 19.6 8 1 ANG2_BOTJA Q10582 bothrops ja
41 11 19.6 8 1 RSI_ERWCH P37985 erwinia chr
42 11 19.6 8 1 UPAL_HUMAN P30087 homo sapien
43 11 19.6 9 1 CONO_CONGE P05486 conus geogr
44 11 19.6 9 1 DCML_PSECF P19913 pseudomonas
45 11 19.6 9 1 OXYA_SCYCA P42996 scyllorhinu

ALIGNMENTS

RESULT 1
ES1_RAT STANDARD; PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=WISTAR; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P2) IS: 8.9, ITS MW IS: 25 kDa.
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 33.9%; Score 19; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 6 KARVOVV 12
Db 1 RARVALV 7

RESULT 2
ULAL_MOUSE STANDARD; PRT; 12 AA.
ID ULAL_MOUSE
AC P99032;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014M9)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 11.7 kDa.
DR SWISS-2DPAGE; P99032; MOUSE.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1324 MW; DD6468EE9F75BAB6 CRC64;

Query Match 30.4%; Score 17; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNVK 5
|||
Db 2 DNVQ 5

RESULT 3
HCYB_MEGCR STANDARD; PRT; 12 AA.
AC Q10584;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemocyanin B chain (KLH-B) (Fragment).
OS Megathura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Fissurellidae; Megathura.
OX NCBI_TaxID=55429;
RN [1]
RP SEQUENCE.
RX MEDLINE=96208935; PubMed=8829804;
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "keyhole limpet hemocyanin: structural and functional
characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -!- SUBUNIT: DIDECAMERS AND EXTENDED MULTIMERS.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: HEMOLYMPH.
CC -!- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
CC protein for haptens and more recently in human vaccines and for
CC immunotherapy of bladder cancer.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR InterPro: IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Oxygen transport; Transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1345 MW; CBFBEAA4A432412 CRC64;

Query Match 28.6%; Score 16; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDNVKKARV 9
:|:|:
Db 1 VDTVVRKNV 9

RESULT 4
CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.

OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
DR KW Oxidoreductase.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVKKAR 8
||:|
Db 1 DNPNSR 7

RESULT 5
RS19_TOBBP STANDARD; PRT; 12 AA.
AC Q36251;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19.
OS Tomato big bud phytoplasma.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Actinobacteria; Actinomycetaceae; Phytoplasma.
OX NCBI_TaxID=35770;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification";
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L27004; AAA83952.1; -
DR InterPro: IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1470 MW; 4CC88BE908333AA3 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 12;
Best Local Similarity 37.5%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 NVKKARVQ 10
||:|:
Db 3 NKDKKMQ 10

RESULT 6
ID ULAD_HUMAN STANDARD; PRT; 9 AA.
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.,
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
DR SWISS-2DPAGE; P31929; HUMAN.
FT NON_TER
SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VKK 6
Db 2 VKK 4

RESULT 7
ID FARP_LOCFI STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistoflrfamide (PDVDFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Acridoidea; Locusta.
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelincx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
(Schistoflrfamide) in Locusta migratoria and its association with the
male accessory glands, the salivary glands, the heart, and the
oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
FMRF-amide-like neuropeptide from the locust, Schistocerca
gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -1- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL

OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -1- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A32543; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDNV 4
Db 3 VDHV 6

RESULT 8
ID LCMS_LEUMA STANDARD; PRT; 10 AA.
AC P21144; P41497;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucomyosuppressin (LMS) (LeM-MS).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberioidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin,
RT an insect neuropeptide that inhibits spontaneous contractions of the
RT cockroach hindgut.";
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -1- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
CC PROTODEUM (HINDGUT).
KW Neuropeptide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDNV 4
Db 3 VDHV 6

RESULT 9
ID NEMS_DROME STANDARD; PRT; 10 AA.
AC P41494;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Dromyosuppressin (Neomyosuppressin) (NEB-MS).
GN DMS OR NEMS.
OS Drosophila melanogaster (Fruit fly), and
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```

OX NCBI_TaxID=7227, 7385;
[1]
RN SEQUENCE.
RC SPECIES=D.melanogaster;
EX MEDLINE=93002195; PubMed=1390001;
RA Nichols R.;
RT "Isolation and structural characterization of Drosophila
RD TDVDFVFLRFamide and FWRamide-containing neural peptides.";
RL J. Mol. Neurosci. 3:213-218(1992).
[2]
RN SEQUENCE.
RC SPECIES=S.bullata; TISSUE=Head;
RX MEDLINE=93047886; PubMed=1358537;
RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
RT "Isolation, primary structure and synthesis of neomyosuppressin, a
RD myoinhibiting neuropeptide from the grey fleshfly, Neobellieria
RL Comp. Biochem. Physiol. 102C:239-245(1992).
CC -!- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
DR FlyBase; FBgn0011581; Dms.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1248 MW; D3C00329D2C1EAB2 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNV 4
DB 3 VDHV 6

RESULT 10
CS15_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RD Submitted (OCT-1997) to the SWISS-PROT data bank.
[2]
RN CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
DR Subtilist; BG7777; ????
KW Complete proteome.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECE6322C330 CRC64;

Query Match 25.0%; Score 14; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NVK 5
DB 3 NIK 5

```

```

RESULT 11
UH11_RAT STANDARD; PRT; 7 AA.
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot p11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.;
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
FT UNSURE 2 2 OR A.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KKARVQ 10
DB 1 QSAREQ 6

RESULT 12
IPYR_RHOVI STANDARD; PRT; 9 AA.
AC P82992;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase) (Fragment).
GN PPA.
OS Rhodospseudomonas viridis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Hyphomicrobium group; Blastochloris.
OX NCBI_TaxID=1079;
[1]
RN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RA Gomez R., Losada M., Serrano A.;
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS PROTEIN IS:
CC 23 kDa.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
DR InterPro; IPR001596; Pyrophosphatase.
DR PROSITE; PS00387; PPASE; PARTIAL.
KW Hydrolase.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1014 MW; 68F3EAA05DDAA044 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDNVKKA 7
DB 3 IDAIDXA 9

```


RESULT 13
RS10_SERMA
ID RS10_SERMA STANDARD; PRT; 9 AA.
AC O68936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RPSJ.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF058451; AAC14294.1; -;
DR InterPro: IPR001848; Ribosomal_S10.
DR PROSITE: PS00361; RIBOSOMAL_S10; PARTIAL.
KW Ribosomal protein.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1214 MW; DE394400416D456 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 9;
Best Local Similarity 12.5%; Pred. No. 1e+05;
Matches 1; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 VKKRVV 11
: : :
DB 1 MNQRI 8

RESULT 14
COXQ_RABIT
ID COXQ_RABIT STANDARD; PRT; 10 AA.
AC P80336;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8H.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
KW Oxidoreductase; Mitochondrion.

FT NON_TER 10
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KKAR 8
: : :
DB 4 KPAR 7

RESULT 15
UXA6_CHLTR
ID UXA6_CHLTR STANDARD; PRT; 10 AA.
AC P38007;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Viret E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Stena-2DPAGE; P38007; -;
FT NON_TER 10
SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VKK 6
: : :
DB 6 IKK 8

RESULT 16
FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 12 AA.
AC P41869;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallimyrFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RL "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callimyrFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; E44787; E44787.

KW Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNV 4
DB 7 DNM 9

RESULT 17
OPS3_DROVI
ID OPS3_DROVI STANDARD; PRT; 12 AA.
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Opsin Rh3 (inner R7 photoreceptor cells opsin) (Fragment).
GN RH3.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Eohydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249748; PubMed=2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals a bipartite organization to rhodopsin promoters in Drosophila melanogaster.";
RL Genes Dev. 4:444-463(1990).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR OMATIDIA. EACH OMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8), THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER CELLS.
CC -!- MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; X51350; CAA35742.1; -
CC GCRDB; GCR 0779; -
CC FlyBase; FBgn0013091; Dvir\Rh3.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC DR PROSITE; PS00237; GPCR_Rhodpsn.
CC DR PROSITE; PS00238; OPSIN; PARTIAL.
CC DR Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
KW Glycoprotein; G-protein coupled receptor; Vision.
FT CARBOHYD 10 10 N-LINKED (GLCNAC...) (PROBABLE).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1253 MW; 04024E43495865B0 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDNV 4
DB 8 IGNV 11

RESULT 18
RS19_CLYEP
ID RS19_CLYEP STANDARD; PRT; 12 AA.
AC Q46490;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19.
OS Clover yellow edge phytoplasm.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Achleplasmataceae; Phytoplasma.
OX NCBI_TaxID=35775;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; L27019; AAA83940.1; -
CC DR InterPro; IPR002222; Ribosomal_S19.
CC DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1409 MW; 4CC478EFC8333AA3 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KKAQVQ 10
DB 5 KDKKIQ 10

RESULT 19
UH03_RAT
ID UH03_RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.

CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.3, ITS MW IS: 28 kDa.

FT UNSURE 2 2
FT UNSURE 9 9
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match 23.28; Score 13; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KARVQV 11
| : | |
Db 5 KIKVAV 10

RESULT 20

FARB_CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR: B44787; B44787.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 926 MW; 69D4069C44AB700 CRC64;

Query Match 21.48; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DN 3
| |
Db 2 DN 3

Search completed: July 8, 2002, 11:48:59
Job time: 330 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:48:39 ; Search time 39.63 Seconds
(without alignments)
52.383 Million cell updates/sec

Title: US-09-461-061A-3
Perfect score: 56
Sequence: 1 IDNVKKARQVV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_TREMBL_19:
2: sp_archaea:
3: sp_bacteria:
4: sp_fungi:
5: sp_human:
6: sp_invertebrate:
7: sp_mammal:
8: sp_mhc:
9: sp_organelle:
10: sp_phase:
11: sp_plant:
12: sp_rodent:
13: sp_virus:
14: sp_vertebrate:
15: sp_unclassified:
16: sp_rviro:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	37.5	12	8 Q37791	Q37791 larix eurol
2	21	37.5	12	8 Q36668	Q36668 pinus sylve
3	20	35.7	11	2 Q9R446	Q9R446 neisseria g
4	20	35.7	11	2 Q44090	Q44090 acholeplasm
5	20	35.7	12	16 Q25179	Q25179 helicobacte
6	18	32.1	10	4 Q9H121	Q9H121 homo sapien
7	18	32.1	10	10 P82434	P82434 nicotiana t
8	17	30.4	8	2 Q9AGP4	Q9AGP4 arthrobacte
9	17	30.4	11	12 Q83083	Q83083 leucania se
10	17	30.4	12	8 P92457	P92457 ephedra sp.
11	16	28.6	8	3 Q05403	Q05403 saccharomyc
12	16	28.6	9	9 Q9XJN0	Q9XJN0 bacterioph
13	16	28.6	10	7 Q95HGO	Q95HGO papio anubi
14	16	28.6	10	7 Q95HF9	Q95HF9 papio anubi
15	16	28.6	10	7 Q95HF7	Q95HF7 papio anubi
16	16	28.6	10	7 Q95HF6	Q95HF6 papio anubi

17	16	28.6	10	7 Q95HF5	Q95HF5 papio anubi
18	16	28.6	10	7 Q95HF4	Q95HF4 papio anubi
19	16	28.6	11	2 Q9R5P3	Q9R5P3 serratia ma
20	16	28.6	11	10 Q82070	Q82070 triticum ae
21	16	28.6	11	12 Q86565	Q86565 varicella-2
22	16	28.6	12	8 Q37790	Q37790 larix eurol
23	16	28.6	12	8 Q36669	Q36669 pinus sylve
24	16	28.6	12	8 Q03815	Q03815 abies alba
25	16	28.6	12	8 Q03816	Q03816 metasequoia
26	16	28.6	12	10 P94011	P94011 arabidopsis
27	15	26.8	7	8 P92421	P92421 psathyrosta
28	15	26.8	7	8 P92385	P92385 hordeum mar
29	15	26.8	7	8 P92372	P92372 haynaldia v
30	15	26.8	7	8 P92403	P92403 lophopyrum
31	15	26.8	7	8 P92425	P92425 pseudoroseg
32	15	26.8	7	8 P92387	P92387 henrardia p
33	15	26.8	7	8 P92427	P92427 peridictyon
34	15	26.8	7	8 P92390	P92390 heteranthel
35	15	26.8	7	8 P92226	P92226 crithopsis
36	15	26.8	7	8 P92214	P92214 amblyopyrum
37	15	26.8	7	8 P92430	P92430 aegilops ta
38	15	26.8	7	8 P92221	P92221 bromus iner
39	15	26.8	7	8 P92442	P92442 taeniatheru
40	15	26.8	7	8 P92381	P92381 hordeum bra
41	15	26.8	7	8 P92393	P92393 hordeum vul
42	15	26.8	7	8 P92218	P92218 australopyr
43	15	26.8	7	8 P92440	P92440 thinopyrum
44	15	26.8	7	8 P92210	P92210 agropyron c
45	15	26.8	7	12 Q9YIR0	Q9YIR0 human adeno

ALIGNMENTS

RESULT 1

Q37791 ID Q37791 PRELIMINARY; PRT; 12 AA.
AC Q37791;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE
DE (FRAGMENT).
GN CHLB.
OS Larix eurolepis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Larix.
OX NCBI_TaxID=49226;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COTYLEDONS;
RA Karpinska B., Karpinski S., Hilgren J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98686; CAA67244.1; -;
DR EMBL; X98681; CAA67239.1; -;
DR EMBL; X98679; CAA67237.1; -;
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 0AB0FC0CC2276724 CRC64;

Query Match 37.5%; Score 21; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDNVKKAR 8

DB 3 LKNLPKAR 10

RESULT 2

Q36668
ID Q36668 PRELIMINARY; PRT; 12 AA.
AC Q36668;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE
DE (FRAGMENT).
OS CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COYLEDONS;
RX MEDLINE=97263785; PubMed=9108142;
RA Karpinska B., Karpinski S., Hallgren J.E.;
RT "The chlB gene encoding a subunit of light-independent
RT protochlorophyllide reductase is edited in chloroplast of conifers.";
RL Curr. Genet. 31:343-347(1997).
DR EMBL; X98683; CAA67240.1; -;
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 0AB0FC0CC2276724 CRC64;

Query Match 37.5%; Score 21; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. NO. 2.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IDNVKAR 8
Db 3 LKNLPKAR 10

RESULT 3
Q9R446 PRELIMINARY; PRT; 11 AA.
ID Q9R446
AC Q9R446;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CARBAMOYL-PHOSPHATE SYNTHASE SUBUNIT A (FRAGMENT).
GN CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, AND FA1090;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billows F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, AND FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029363; AAC78453.1; -;
DR EMBL; AF029362; AAC78452.1; -;
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DD33694 CRC64;

Query Match 35.7%; Score 20; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. NO. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IDNVKAR 8
Db 2 IGNMKAAR 9
RESULT 4
Q44090 PRELIMINARY; PRT; 11 AA.
ID Q44090
AC Q44090;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL EXPORT SEGMENT (FRAGMENT).
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
RT beta-lactamase in Escherichia coli.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z22875; CAA80495.1; -;
FT NON_TER 11 11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 35.7%; Score 20; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. NO. 3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VKKARVQVV 12
Db 1 MKKLKVMTV 9

RESULT 5
O25179 PRELIMINARY; PRT; 12 AA.
ID O25179
AC O25179;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 1.4 KDA PROTEIN.
GN HP0429.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., B.A.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000559; AAD07512.1; -;
DR TIGR; HP0429; -;
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 12 AA; 1375 MW; 20959A84E2133338 CRC64;

Query Match 35.7%; Score 20; DB 16; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVKKARQV 11
:| | | :|
Db 3 ENGRKEALQL 12

RESULT 6
Q9H121 ID Q9H121 PRELIMINARY; PRT; 10 AA.
AC Q9H121;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ309F20.1.2 (ISOFORM 2 OF GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA STIMULATING ACTIVITY POLYPEPTIDE 1) (FRAGMENT).
GN GNAS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL121917; CAC18783.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1095 MW; 7809E3D322C7244B CRC64;

Query Match 32.1%; Score 18; DB 4; Length 10;
Best Local Similarity 42.9%; Pred. No. 6.3e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IDNVKKA 7
:| | :|
Db 2 LENLVKA 8

RESULT 7
P82434 ID P82434 PRELIMINARY; PRT; 10 AA.
AC P82434;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 28 KDA CELL WALL PROTEIN (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RN SEQUENCE.
RP STRAIN=CV. PETIT HAVANA;
RC Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture."
RL Planta 0:0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1054 MW; 1A4B96DDAB2C444 CRC64;

Query Match 32.1%; Score 18; DB 10; Length 10;

Best Local Similarity 57.1%; Pred. No. 6.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DNVKKAR 8
:| | :|
Db 3 NNVDAAAR 9

RESULT 8
Q9AGP4 ID Q9AGP4 PRELIMINARY; PRT; 8 AA.
AC Q9AGP4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SERINE HYDROXYMETHYLTRANSFERASE (FRAGMENT).
GN GLYA.
OS Arthrobacter sp. LIN.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=153502;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=LIN;
RC Meskys R., Harris R.J., Casate V., Basran J., Scrutton N.S.;
RA "Genetic organization of the genes involved in dimethylglycine and sarcosine degradation in Arthrobacter spp.: implications for glycine betaine catabolism."
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF329478; AAK16486.1; -
DR EMBL: AF329478; AAK16486.1; -
KW Transferase; Methyltransferase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 898 MW; 6B18705333372457 CRC64;

Query Match 30.4%; Score 17; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NVKK 6
:| | :|
Db 2 NLKK 5

RESULT 9
Q83083 ID Q83083 PRELIMINARY; PRT; 11 AA.
AC Q83083;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P13 MINI PEPTIDE.
OS Leucania separata nuclear polyhedrosis virus (LsNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=41714;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96140622; PubMed=8572949;
RX Wang J.W., Qi Y.P., Huang Y.X., Li S.D.;
RA "Nucleotide sequence of a 1446 base pair Sali fragment and structure of a novel early gene of Leucania separata nuclear polyhedrosis virus."
RT Arch. Virol. 140:2283-2291(1995).
RL EMBL: U30303; AAA99737.1; -
DR EMBL: U30303; AAA99737.1; -
SQ SEQUENCE 11 AA; 1339 MW; F7BDE0BD40DC401 CRC64;

Query Match 30.4%; Score 17; DB 12; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVKKARV 9

Db 2 NRHRARV 8

RESULT 10
P92457 PRELIMINARY; PRT; 12 AA.

ID P92457 AC P2457;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DRC-2001 (TREMBLrel. 19, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE (FRAGMENT).
DE CHLB GENE.
OS Ehedra sp.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnetales; Gnetales; Ephedrales; Ephedraceae;
OC Ephedra.
OX NCBI_TaxID=41991;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263785; PubMed=9108142;
RA Karpinska B., Karpinski S., Hallgren J.E.;
RT "The chlB gene encoding a subunit of light-independent
RT protochlorophyllide reductase is edited in chloroplast of conifers.";
RL Curr. Genet. 31:343-347(1997).
DR EMBL; X98573; CAA67182.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1441 MW; 164C1B7CC2276724 CRC64;

Query Match 30.4%; Score 17; DB 8; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.2e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDNVKKA 7
Db 3 LQNLPKA 9

RESULT 11
Q05403 PRELIMINARY; PRT; 8 AA.

ID Q05403 AC Q05403;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DNA FOR ORF'S FROM CHROMOSOME XV (FRAGMENT).
GN COO3 AND YOL096C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FYL1679;
RA MEDLINE=96021609; PubMed=8533473;
RZ Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
DR SGD; S0003456; COQ3.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 28.6%; Score 16; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDNVKK 6
Db 2 IHNVVK 7

RESULT 12
Q9XJN0 PRELIMINARY; PRT; 9 AA.

ID Q9XJN0 AC Q9XJN0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE P10 (FRAGMENT).
OS bacteriophage phi-10.
OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX NCBI_TaxID=90889;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99350412; PubMed=10419946;
RA Mindich L., Qiao X., Qiao J., Romantschuk M.,
RA Hoogstraaten D.;
RT "Isolation of additional bacteriophages with genomes of segmented
RT double-stranded RNA.";
RL J. Bacteriol. 181:4505-4508(1999).
DR EMBL; AF125675; AAD22555.1; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;

Query Match 28.6%; Score 16; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. NO. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNV 4
Db 1 MDNI 4

RESULT 13
Q95HG0 PRELIMINARY; PRT; 10 AA.

ID Q95HG0 AC Q95HG0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN PAAN-AG.
OS Papio anubis (olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=HEART;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RT from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055032; AAL23590.1; -.
FW MHC.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. NO. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NVKKA 7
Db 1 NMKN 5


```

RESULT 14
Q95HF9 ID Q95HF9 PRELIMINARY; PRT; 10 AA.
AC Q95HF9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055033; AAL23591.1; -.
KW MHC.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVKKA 7
Db 1 NMKNA 5

RESULT 15
Q95HF7 ID Q95HF7 PRELIMINARY; PRT; 10 AA.
AC Q95HF7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055035; AAL23593.1; -.
KW MHC.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVKKA 7
Db 1 NMKNA 5

```

```

RESULT 16
Q95HF6 ID Q95HF6 PRELIMINARY; PRT; 10 AA.
AC Q95HF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055036; AAL23594.1; -.
KW MHC.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVKKA 7
Db 1 NMKNA 5

RESULT 17
Q95HF5 ID Q95HF5 PRELIMINARY; PRT; 10 AA.
AC Q95HF5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055037; AAL23595.1; -.
KW MHC.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVKKA 7
Db 1 NMKNA 5

```

RESULT 18

Q95HF4 ID Q95HF4 PRELIMINARY; PRT; 10 AA.
 AC Q95HF4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN PAAN-AG.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYMUS;
 RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
 RT "The baboon placenta contains unique tissue-specific messages derived
 from the class Ib major histocompatibility complex gene, Paan-AG.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY055038; AAL23596.1; -
 KW MHC.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 28.6%; Score 16; DB 7; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVKKA 7
 I: I
 Db 1 NMKNA 5

RESULT 19

Q9R5P3 ID Q9R5P3 PRELIMINARY; PRT; 11 AA.
 AC Q9R5P3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE SM2=NUCLEASE.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92134331; PubMed=1663739;
 RA Bannikova G.E., Blagova E.V., Dementiev A.A., Morgunova E.Yu.,
 RA Mikhailov A.M., Shiyapnikov S.V., Varlamov V.P., Vainshtein B.K.;
 RT "Two isoforms of Serratia marcescens nuclease. Crystallization and
 preliminary x-ray investigation of the enzyme.";
 RL Biochem. Int. 24:813-822(1991).
 SQ SEQUENCE 11 AA; 1179 MW; 6DF18EE04AA045BB CRC64;

Query Match 28.6%; Score 16; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDN 3
 I: I
 Db 6 IDN 8

RESULT 20

O82070 ID O82070 PRELIMINARY; PRT; 11 AA.
 AC O82070;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RNA POLYMERASE (EC 2.7.7.6) (FRAGMENT).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CHINESE SPRING;
 RA Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;
 RT "Characterization of a gene encoding a single-subunit RNA polymerase
 from maize which is alternatively spliced.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ005344; CAA06489.1; -
 KW Transferase; Nucleotidyltransferase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 28.6%; Score 16; DB 10; Length 11;
 Best Local Similarity 30.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDNVKARVQ 10
 I: I: I:
 Db 1 VDEVDRKLVK 10

Search completed: July 8, 2002, 11:48:40
 Job time: 336 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:42:57 ; Search time 48.86 Seconds
(without alignments)
27.280 Million cell updates/sec

Title: US-09-461-061A-3

Perfect score: 56

Sequence: 1 IDNVKKARQVQV 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 158732

Minimum DB seq length: 10

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*

1: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseg/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	12	21	AA195407
2	30	53.6	11	21	AA195407
3	26	46.4	8	21	AA195407
4	26	46.4	12	19	AA195407
5	24	42.9	11	22	AA195407
6	24	42.9	12	16	AA195407
7	23	41.1	7	14	AA195407
8	23	41.1	8	22	AA195407
9	23	41.1	8	22	AA195407
10	23	41.1	8	22	AA195407
11	23	41.1	9	20	AA195407
					Anti-angiogenic peptide C-terminal fragment.
					Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
					endothelial cell proliferation; apoptosis; cancer; ocular disorder;
					rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
					therapy; human; D3 peptide.
					Homo sapiens.
					WO200035407-A2.
					22-JUN-2000.
					02-DEC-1999; 99WO-US28465.
					16-DEC-1998; 98US-0112427.
					(UTEM) UNIV TEMPLE.
					(MCCR/) MCCRAE R K.
					McCrae RK;
					WPI; 2000-442247/38.
					Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer,

12	23	41.1	10	22	AAU07043	Human MHC molecule
13	23	41.1	11	15	AARS4725	ScFv-Ad5 fusion pr
14	23	41.1	12	20	AAV01108	HBGF-0.8-p2 peptid
15	23	41.1	12	20	AAW89521	Human latent trans
16	23	41.1	12	21	AAAB15882	Human chemokine de
17	23	41.1	12	21	AAV78078	Human lactoferrin
18	22	39.3	8	14	AAV43470	Ro/SSA epitope 315
19	22	39.3	8	22	AAE08182	Peptide #81 from h
20	22	39.3	9	16	AAV75015	Deletion mutant de
21	22	39.3	10	19	AAW64638	Synthetic SB pept
22	22	39.3	10	22	AAAG3000	Mycoplasma genital
23	22	39.3	10	22	AAAG8264	Saccharomyces cere
24	22	39.3	11	22	AAE05947	Basic aminooxyacet
25	22	39.3	12	16	AAV75020	Deletion mutant de
26	22	39.3	12	18	AAW35174	Lys/Val diastereom
27	22	39.3	12	18	AAW35175	Lys/Val diastereom
28	22	39.3	12	18	AAW35176	Lys/Val diastereom
29	22	39.3	12	19	AAW82890	Antipathogenic pep
30	22	39.3	12	19	AAW82891	Antipathogenic pep
31	22	39.3	12	19	AAW82892	Antipathogenic pep
32	22	39.3	12	21	AAAB17425	Antipathogenic pep
33	22	39.3	12	21	AAAB17427	Antipathogenic pep
34	22	39.3	12	21	AAV78083	Antipathogenic pep
35	22	39.3	12	21	AAV78086	Human lactoferrin
36	21	37.5	6	9	AAV81903	A second minor try
37	21	37.5	7	22	AAW44081	H11 binding site c
38	21	37.5	7	22	AAW44086	H11 binding site c
39	21	37.5	7	22	AAW44092	H11 binding site c
40	21	37.5	7	22	AAW44172	H11 binding site c
41	21	37.5	7	22	AAW44177	H11 binding site c
42	21	37.5	7	22	AAW44675	H11 binding site c
43	21	37.5	7	22	AAW44678	H11 binding site c
44	21	37.5	7	22	AAW44685	H11 binding site c
45	21	37.5	7	22	AAW45852	H11 binding site c

ALIGNMENTS

RESULT 1

AA195407

ID AA195407 standard; Peptide; 12 AA.

XX AA195407;

XX AC AA195407;

XX DT 25-SEP-2000 (first entry)

XX DE Anti-angiogenic peptide C-terminal fragment.

XX KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

XX KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

XX KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;

XX KW therapy; human; D3 peptide.

XX OS Homo sapiens.

XX PN WO200035407-A2.

XX PD 22-JUN-2000.

XX PF 02-DEC-1999; 99WO-US28465.

XX PR 16-DEC-1998; 98US-0112427.

XX PA (UTEM) UNIV TEMPLE.

XX PA (MCCR/) MCCRAE R K.

XX PI McCrae RK;

XX DR WPI; 2000-442247/38.

XX PT Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer,

PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog
PS
PS Claim 3; Page 25; 44pp; English.
XX
XX The present sequence is that of a C-terminal fragment of a novel
CC anti-angiogenic D3 peptide (see AAY95408) derived from human high
CC mol.wt. kininogen (HK) domain 3 (see AAY95426). The full-length D3
CC peptide inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of peptides of the
CC invention (see AAY95405-26) that are analogues of certain sites in
CC the HK domain 3. The peptides inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.
XX
XX Sequence 12 AA;
SQ

Query Match 100.0%; Score 56; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNVKKARQVV 12
Db 1 IDNVKKARQVV 12
|||||
|

RESULT 2
ID AAB26620 standard; Peptide; 11 AA.
XX
AC AAB26620;
XX
XX 22-JAN-2001 (first entry)
XX
DE Partial sequence #20 of Breast Cancer-Associated Protein Isoform.
XX BPI; breast cancer-associated protein isoform; gene therapy;
KW breast cancer.
XX
XX Homo sapiens.
XX WO200055628-A1.
PN
XX 21-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-GB00908.
XX
PR 12-MAR-1999; 95GB-0005817.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Amess B, Townsend RR, Parekh RB, Waterfield MD, O'Hare MJ;
XX WPI; 2000-602142/57.
DR
XX Screening, diagnosis of breast cancer and monitoring the effectiveness
PT of breast cancer therapy, involves detecting breast cancer-associated
PT features and breast cancer-associated protein isoforms -
XX
PS Disclosure; Page 13; 86pp; English.
XX
XX The present invention relates to the screening, diagnosis and prognosis
CC of breast cancer, for monitoring the effectiveness of breast cancer
CC treatment in a human, comprising identifying the presence or absence
CC of breast cancer-associated features (BF) or breast cancer-associated
CC protein isoforms (BPIs). Antibodies derived from BF and BPIs may be
CC useful for the treatment and screening of breast cancer, in particular
CC metastatic breast cancer. The present sequence is the partial

CC sequence of a BPI.
XX
SQ Sequence 11 AA;

Query Match 53.6%; Score 30; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNVKK 6
Db 6 IDNVKK 11
|||||
|

RESULT 3
ID AAB08552 standard; Peptide; 8 AA.
XX
AC AAB08552;
XX
XX 20-DEC-2000 (first entry)
XX
DE Peptide identified from an origin of prepro-bradykinine.
XX
KW Precursor peptide; polypeptide hormone; peptide identification.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "hydrogen attached"
FT Modified-site 8 /note= "amidated residue"
XX
XX WO200050636-A1.
XX
XX 31-AUG-2000.
XX
XX 24-FEB-2000; 2000WO-FR00460.
XX
XX 25-FEB-1999; 99US-0257525.
XX
XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Camara Ferrer YJA, Thuriereau C, Martinez J, Berge G, Goze C;
XX WPI; 2000-572101/53.
DR
XX Identifying peptide with selected function, useful particularly for
PT C-amidated hormones, by screening database for combination of nucleic
PT acid and amino acid sequences -
XX
XX Claim 16; Page 20; 40pp; French.
XX
XX The specification describes a method for identifying a peptide having
CC a particular function. The method comprises preparing a database of
CC polynucleotides and polypeptides of unknown functions, screening the
CC database for a combination of nucleotides or amino acids indicative of
CC the peptide with a particular function, and identifying polynucleotides
CC and proteins which contain the peptide. The method is used to identify
CC precursor peptides with an amidated C-terminus, especially polypeptide
CC hormones, for studying physiologically active substances. The present
CC sequence represents a peptide which was identified using the method of
CC the invention.
XX
SQ Sequence 8 AA;

Query Match 46.4%; Score 26; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ARVQVV 12
Db 2 arvqv 7

RESULT 4

AAW64637
ID AAW64637 standard; peptide; 12 AA.

XX AC AAW64637;
XX DT 23-OCT-1998 (first entry)

XX DE Synthetic SEB peptide p12(151-161).

XX KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
XX KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
XX KW therapeutic; vaccine; food poisoning.

XX OS Synthetic.
XX OS Staphylococcus aureus.

XX PN WO9829444-A1.

XX PD 09-JUL-1998.

XX PF 30-DEC-1997; 97WO-IL00438.

XX PR 30-DEC-1996; 96IL-0119938.

XX PA (YISS) YISSUM RES & DEV CO.

XX PI Arad G, Kaempfer R;

XX DR WPI; 1998-388042/33.

XX XX New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s)
XX XX Claim 8; Page 41; 68pp; English.

XX XX AAW64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide.
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or
CC TNF-beta genes. The peptides may be used to prepare therapeutics or
CC vaccines for the treatment of prophylaxis of toxin-mediated activation
CC of T cells and eliciting protective immunity against toxic shock induced
CC by PETs. They can also be used for the treatment of harmful effects
CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
CC the peptides can also be used for alleviating toxic shock induced by
CC PET.

XX SQ Sequence 12 AA;

Query Match 46.4%; Score 26; DB 19; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 NVKKARVQ 10
Db 2 nkkkatv 9

RESULT 5

AAE12505

ID AAE12505 standard; peptide; 11 AA.

XX XX
AC AAE12505;

XX 03-JAN-2002 (first entry)

XX DE Membrane transiting antiviral peptide P22.

XX KW Membrane transiting peptide; virucide; antiviral; Herpes Simplex Virus;
XX KW HSV; HIV; Human Immunodeficiency Virus; CMV; cytomegalovirus.

XX OS Unidentified.

XX PN WO200157072-A2.

XX PD 09-AUG-2001.

XX PF 06-FEB-2001; 2001WO-US03813.

XX PR 07-FEB-2000; 2000US-180823P.

XX PR 22-FEB-2000; 2000US-184057P.

XX PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX PI Brandt C, Bultmann H;

XX DR WPI; 2001-638840/73.

XX XX Peptides comprising membrane transiting peptides useful for treating or
PT preventing a virus infection, e.g., human immunodeficiency virus,
PT herpes simplex virus and cytomegalovirus -

XX PS Claim 7; Page 7; 43pp; English.

XX XX The invention relates to peptides comprising membrane transiting
CC peptides with antiviral properties. The peptides are useful for
CC treating or preventing a virus infection in a warm blooded animal,
CC e.g., enveloped viruses such as human immunodeficiency virus (HIV),
CC herpes simplex virus (HSV), cytomegalovirus (CMV) and non-enveloped
CC virus. Preferably, the peptides are useful for treating or preventing
CC infections from one or more HSVs. The antiviral peptides are used for
CC treating viral infections of the skin or part of the oral or genital
CC cavity. The present sequence is membrane transiting antiviral peptide.

XX SQ Sequence 11 AA;

Query Match 42.9%; Score 24; DB 22; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 KKARVQVV 12
Db 3 kkaavav 10

RESULT 6

AAR82025

ID AAR82025 standard; Peptide; 12 AA.

XX AC AAR82025;

XX DT 10-APR-1996 (first entry)

XX DE Stearoyl-ACP-desaturase N-terminal peptide (aa5-16).

XX KW Stearoyl-ACP-desaturase; soybean; seed oil; vegetable oil;
XX KW fatty acid; stearic acid; transgenic plant; crop improvement..

XX OS Synthetic.

XX PN US5443974-A.

XX PD 22-AUG-1995.

XX PF 25-MAY-1990; 90US-0529049.

XX 11-DEC-1992; 92US-0995657.
PR 25-MAY-1990; 90US-0529049.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Hitz WD, Perez-Grau L, Yadav NS;
XX WPI; 1995-302121/39.
XX New isolated soybean stearyl-ACP desaturase gene - use for the
PT prodn. of seed oil contg. altered levels of satd. and unsatd. fatty
PT acids
XX PS Disclosure; Column 43-44; 25pp; English.
XX Amino acids 5-16 (AAR82025) of the soybean leaf stearyl-ACP-
CC desaturase mature enzyme were used to design a set of degenerate
CC DNA probes (AAT00401). The probes were utilized in the screening of
CC soybean leaf cDNA expression libraries, leading to the isolation of
CC a clone (AAT00395) coding for the precursor enzyme (AAR82024).
XX SQ Sequence 12 AA;
Query Match 42.9%; Score 24; DB 16; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 IDNVKK 6
Db 3 venikk 8
RESULT 7
AAR43469
ID AAR43469 standard; peptide; 7 AA.
XX AC AAR43469;
XX 12-MAY-1994 (first entry)
DE Ro/SSA epitope 313.
XX Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;
KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;
KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';
KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.
XX OS Homo sapiens.
XX WO9321223-A.
XX 28-OCT-1993.
XX 13-APR-1993; 93WO-US03484.
XX 13-APR-1992; 92US-0867819.
XX (OKLA) UNIV OKLAHOMA STATE.
XX Harley JB;
XX WPI; 1993-351658/44.
XX New linear epitope(s) for human auto-antibodies - from the
PT Ro/SSA, La/SSB and Sm B/B' antigens and ribonucleoprotein, used
PT for diagnosing and treating auto-immune disorders e.g. systemic
PT lupus erythematosus
XX Claim-1; Page 31; 43pp; English.
XX The sequences given in AAR43391-562 are linear epitopes which are

CC derived from the 60 kD Ro/SSA peptide, the La/SSB autoantigen,
CC the 70 kD nuclear ribonucleoprotein (nRNP) and the Sm B/B',
CC polypeptide. These antigens are common in systemic lupus
CC erythematosus (SLE) and closely related disorders. The Ro/SSA family
CC of proteins has been shown to have several molecular forms which are
CC defined by the molecular weight of the antigen identified. The major
CC form has a molecular weight of 60 kD and two additional forms have
CC molecular weights of 52 and 54 kD. La/SSB is also a member of this
CC group of autoantibodies and binds small RNAs with a polypyridine
CC terminus. La/SSB is bound by a third of the anti-Ro/SSA precipitin
CC positive sera. La/SSB has been shown to be a 46-50 kD monomeric
CC phosphoprotein which associates with RNA polymerase III transcripts.
CC Anti-Sm antibodies precipitate snRNPs containing the U1, U2, U4/U6 and
CC U5 RNA. Anti-Sm antibodies may be directed against one or a
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD),
CC E/F (11 kD doublet) and G (less than 10 kD). These epitopes may be
CC used for preventing, treating or screening autoimmune disorders,
CC especially SLE or Sjogrens syndrome (SS). They bind to a human
CC autoantibody and may therefore be used as vaccines.
XX SQ Sequence 7 AA;
Query Match 41.1%; Score 23; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 6.4e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 VKKRV 9
Db 2 lkkari 7
RESULT 8
AAR08179
ID AAR08179 standard; peptide; 8 AA.
XX AC AAR08179;
XX 01-NOV-2001 (first entry)
DE Peptide #78 from human ribonucleoprotein, 60 kD Ro/SSA.
XX Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX OS Homo sapiens.
XX US6232522-B1.
XX 15-MAY-2001.
XX 30-NOV-1993; 93US-0160604.
XX 31-JAN-1990; 90US-0472947.
XX 31-JAN-1991; 91US-0648205.
XX 13-APR-1992; 92US-0867819.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX Harley JB, James JA, Scofield RH;
XX WPI; 2001-335087/35.
XX Generating systemic lupus erythematosus animal model by immunizing
PT non-human animal with non-immunoglobulin peptide having amino acid
PT sequence of self-antigen bound by autoantibody population in early
PT stage of disease -
XX Example 1; Column 16; 63pp; English.
XX The patent discloses a specific method of generating an animal model
CC of systemic lupus erythematosus (SLE), comprising immunising a non-
CC human animal with non-immunoglobulin peptide which comprises an

CC epitope immunoreactive with auto-antibody (AAb) from patient with
 CC SLE. The epitope includes a region of self-antigen which is bound
 CC by AAb population present in early stage in patient with SLE. The
 CC method is used for generating an animal model of SLE. It is useful
 CC for screening therapeutics effective in treating autoimmune disorders.
 CC It is useful as a component in a diagnostic assay, as a therapeutic
 CC (vaccine to block the AAbs produced, by eliciting immune response),
 CC and in research on the possible causes of the autoimmune diseases.
 CC The method is used to interrupt the course of an autoimmune response,
 CC once autoimmunity against the autoantigen is established. The amino
 CC acid sequences are used to make agents for neutralising circulating
 CC antibodies or immobilised on substrates in extracorporeal devices for
 CC specific removal of AAbs. The reagents identified by using the method
 CC are useful in manufacturing and testing autoantigens. The method is
 CC useful as models for screening of compounds which induce autoimmunity,
 CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of
 CC autoimmune disorders. The present sequence is a peptide from human ribo-
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
 CC of the invention.
 CC
 XX
 SQ Sequence 8 AA;

Query Match 41.1%; Score 23; DB 22; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VKKARV 9
 :||||:
 Db 3 lkkari 8

RESULT 9
 AAE08180
 ID AAE08180 standard; peptide; 8 AA.

AC AAE08180;

DT 01-NOV-2001 (first entry)

DE Peptide #79 from human ribonucleoprotein, 60 kD Ro/SSA.

KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
 KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.

OS Homo sapiens.

PN US6232522-B1.

PD 15-MAY-2001.

PF 30-NOV-1993; 93US-0160604.

PR 31-JAN-1990; 90US-0472947.

PR 31-JAN-1991; 91US-0648205.

PR 13-APR-1992; 92US-0867819.

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PI Harley JB, James JA, Scofield RH;

DR WPI; 2001-335087/35.

XX Generating systemic lupus erythematosus animal model by immunizing
 PT non-human animal with non-immunoglobulin peptide having amino acid
 PT sequence of self-antigen bound by autoantibody population in early
 PT stage of disease -

PS Example 1; Column 16; 63pp; English.

XX The patent discloses a specific method of generating an animal model
 CC of systemic lupus erythematosus (SLE), comprising immunising a non-

CC human animal with non-immunoglobulin peptide which comprises an
 CC epitope immunoreactive with auto-antibody (AAb) from patient with
 CC SLE. The epitope includes a region of self-antigen which is bound
 CC by AAb population present in early stage in patient with SLE. The
 CC method is used for generating an animal model of SLE. It is useful
 CC for screening therapeutics effective in treating autoimmune disorders.
 CC It is useful as a component in a diagnostic assay, as a therapeutic
 CC (vaccine to block the AAbs produced, by eliciting immune response),
 CC and in research on the possible causes of the autoimmune diseases.
 CC The method is used to interrupt the course of an autoimmune response,
 CC once autoimmunity against the autoantigen is established. The amino
 CC acid sequences are used to make agents for neutralising circulating
 CC antibodies or immobilised on substrates in extracorporeal devices for
 CC specific removal of AAbs. The reagents identified by using the method
 CC are useful in manufacturing and testing autoantigens. The method is
 CC useful as models for screening of compounds which induce autoimmunity,
 CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of
 CC autoimmune disorders. The present sequence is a peptide from human ribo-
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
 CC of the invention.
 CC
 XX
 SQ Sequence 8 AA;

Query Match 41.1%; Score 23; DB 22; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VKKARV 9
 :||||:
 Db 2 lkkari 7

RESULT 10
 AAE08181
 ID AAE08181 standard; peptide; 8 AA.

AC AAE08181;

DT 01-NOV-2001 (first entry)

DE Peptide #80 from human ribonucleoprotein, 60 kD Ro/SSA.

XX Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
 KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.

OS Homo sapiens.

PN US6232522-B1.

PD 15-MAY-2001.

PF 30-NOV-1993; 93US-0160604.

PR 31-JAN-1990; 90US-0472947.

PR 31-JAN-1991; 91US-0648205.

PR 13-APR-1992; 92US-0867819.

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PI Harley JB, James JA, Scofield RH;

DR WPI; 2001-335087/35.

XX Generating systemic lupus erythematosus animal model by immunizing
 PT non-human animal with non-immunoglobulin peptide having amino acid
 PT sequence of self-antigen bound by autoantibody population in early
 PT stage of disease -

PS Example 1; Column 16; 63pp; English.

XX The patent discloses a specific method of generating an animal model

CC of systemic lupus erythematosus (SLE), comprising immunising a non-
 CC human animal with non-immunoglobulin peptide which comprises an
 CC epitope immunoreactive with auto-antibody (AAb) from patient with
 CC SLE. The epitope includes a region of self-antigen which is bound
 CC by AAb population present in early stage in patient with SLE. The
 CC method is used for generating an animal model of SLE. It is useful
 CC for screening therapeutics effective in treating autoimmune disorders.
 CC It is useful as a component in a diagnostic assay, as a therapeutic
 CC (vaccine to block the AAbs produced, by eliciting immune response),
 CC and in research on the possible causes of the autoimmune diseases.
 CC The method is used to interrupt the course of an autoimmune response,
 CC once autoimmunity against the autoantigen is established. The amino
 CC acid sequences are used to make agents for neutralising circulating
 CC antibodies or immobilised on substrates in extracorporeal devices for
 CC specific removal of AAbs. The reagents identified by using the method
 CC are useful in manufacturing and testing autoantigens. The method is
 CC useful as models for screening of compounds which induce autoimmunity,
 CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of
 CC autoimmune disorders. The present sequence is a peptide from human ribo-
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
 CC of the invention.

XX Sequence 8 AA;

Query Match 41.1%; Score 23; DB 22; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VKKARV 9
 :|||||
 Db 1 lkkari 6

RESULT 11

AAU01110
 ID AAU01110 standard; peptide; 9 AA.

XX AAU01110;

XX 24-MAY-1999 (first entry)

XX CTGF peptide fragment (residues 247-255).

XX Heparin-binding growth factor; HBGF; connective tissue growth factor;
 KW CTGF; pharmaceutical; wound healing; tissue formation; sclerotic; burn;
 KW cell proliferative disorder; atherosclerosis; fibrotic; arthritis; IGF-1;
 KW osteoporosis; skeletal disorder; scleroderma; liver cirrhosis; PDGF;
 KW insulin-like growth factor; platelet-derived growth factor; TGF-beta;
 KW EGF; epidermal growth factor; transforming growth factor beta; bFGF;
 KW basic fibroblast growth factor; heparin; growth; placental membrane;
 KW endometrial growth; pregnancy; endometrial-trophoblast interaction.

XX Synthetic.

XX WO9907407-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16423.

XX 07-AUG-1997; 97US-0908526.

XX (CHIL-) CHILDRENS HOSPITAL RES FOUND.

XX Brigstock DA, Harding PA;

XX WPI; 1999-167214/14.

XX New substantially pure heparin-binding growth factor polypeptides -
 PT useful for affecting wound healing and tissue formation, where
 PT antagonists of the polypeptides are useful for, e.g. treating

PT sclerotic or cell proliferative disorders
 XX
 PS Example 5; Page 33; 53pp; English.

XX The invention relates to a substantially pure heparin-binding growth
 CC factor (HBGF) polypeptide (1 kDa) that corresponds to the C-terminal end
 CC of a connective tissue growth factor (CTGF) protein. The HBGF
 CC polypeptides form pharmaceutical compositions for affecting wound
 CC healing and tissue formation. Antagonists of the polypeptides are useful
 CC for treating sclerotic or cell proliferative disorders, atherosclerosis
 CC or fibrotic conditions. Diseases and conditions modulated by HBGF
 CC include arthritis, osteoporosis, and other skeletal disorders, burns.
 CC Fibrotic conditions include scleroderma, arthritis and liver cirrhosis.
 CC Cells treated are selected from epithelial (especially secretory),
 CC muscle (especially smooth or cardiac muscle), connective tissue
 CC (especially astroglia, fibroblast, osteoclast, osteoblast or chondrocyte
 CC cells) and endothelial (especially endothelial) cells. Each treatment may
 CC further comprise the use of growth factors selected from insulin-like
 CC growth factor (IGF-I), platelet-derived growth factor (PDGF), epidermal
 CC growth factor (EGF), transforming growth factor beta (TGF-beta) or basic
 CC fibroblast growth factor (bFGF). The biological effect of HBGF can be
 CC modulated using heparin at a concentration of 1-100 mg/ml. HBGF is used
 CC for promoting endometrial growth and development of placental membranes
 CC and promoting and maintaining pregnancy by facilitating endometrial-
 CC trophoblast interaction. Sequences AAU01110-127 represent synthetic CTGF
 XX peptide fragments.

XX Sequence 9 AA;

Query Match 41.1%; Score 23; DB 20; Length 9;
 Best Local Similarity 42.9%; Pred. No. 6.4e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNKKAR 8

Db 2 enikkkg 8

RESULT 12

AAU07043

ID AAU07043 standard; Peptide; 10 AA.

XX AAU07043;

XX 24-OCT-2001 (first entry)

XX Human MHC molecule HLA-B3501 binding 84P2A9 peptide #51.

XX 84P2A9-related protein; prostate; testis; tissue; cancer; leukaemia;
 KW tumour; kidney; brain; bone; skin; ovary; breast; pancreas; colon; lung;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood;
 KW single chain monoclonal antibody; urine.

XX Homo sapiens.

XX WO200155391-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02651.

XX 26-JAN-2000; 2000US-0178560.

XX (UROG-) UROGENESYS INC.

XX Jakobovits A, Afar DEH, Challita-eid PM, Levin E, Mitchell SC;
 PI Hubert RS;

XX WPI; 2001-502631/55.

XX New 84P2A9 gene and its encoded protein, useful for diagnosing and
 PT treating cancer, e.g. leukaemia and cancer of the prostate, testis,

PT kidney, brain or bone, or for eliciting an immune response -
XX
PS
XX
XX Example 12; Page 114; 149pp; English.

CC The polypeptide sequences represent the 84P2A9-related protein and
CC peptide fragments of the protein. 84P2A9 exhibits prostate and testis
CC specific expression in normal adult tissue, but it is also aberrantly
CC expressed in many cancers including leukaemia and tumours of the
CC prostate, testis, kidney, brain, bone, skin, ovary, breast, pancreas,
CC colon and lung. The 84P2A9 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 84P2A9-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 84P2A9 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 84P2A9. The sequences can be used in diagnostic methods to
CC monitor the level of 84P2A9 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

Query Match 41.1%; Score 23; DB 22; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VKKARVQV 12
||| :||:
Db 2 vkkrklkii 10

RESULT 13

AAR54725
ID AAR54725 standard; Protein; 11 AA.

XX AC AAR54725;

DT 02-DEC-1994 (first entry)

XX SCFV-Ad5 fusion protein C.

XX Single chain Fv fragment; SCFV; Gene Therapy; Adenovirus;
XX Penton fibre; Ad5; Fusion sites.

OS Adenovirus (Ad5).

XX Key Location/Qualifiers
FH Peptide 1..6

FT /label= Ad5 fibre

FT Peptide 7..10

FT /label= SCFV fragment

FT Misc-difference 11

FT /label= X represents the remainder of the SCFV
FT fragment.

XX W09410323-A.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-GB02267.

XX 04-NOV-1992; 92GB-0023084.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX Epenetos AA, Spooner RA;

XX WPI; 1994-167477/20.

XX N-PSDB; AAQ64764.

XX Virus with modified binding moiety specific for the target cells
PT - used to deliver genes for gene therapy and cancer treatment

XX Example 1; Page 46; 110pp; English.

XX Displaying functional antibody fragments on the surface of
XX recombinant retroviral particles could be used to target replication
XX deficient virus to target cells for gene delivery. The
XX binding moiety (eg. a SCFV) is pref. external to the receptor for
XX its host cell and fused to the virus direct or indirect by a spacer
XX group. The binding site on the target cell is a cell specific
XX antigen. Fusion C (AAQ64764 fused to AAQ64761) is at the end of the
XX third repetitive unit of the shaft (co-ordinates 31323-4 (sequence
XX co-ordinates taken from ADRCOMPGE.1) of the Ad5 fibre. The sequence
XX between the PstI and XhoI sites is unique to the SCFV used. The first 6
XX amino acid residues of the fusion A protein are from Ad5, the next
XX 4 from the SCFV fragment used. X11 represents the remainder of the
XX SCFV used.

SQ Sequence 11 AA;

Query Match 41.1%; Score 23; DB 15; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VKKARVQV 11

Db 2 lkktkvql 9

RESULT 14

AAY01108

ID AAY01108 standard; peptide; 12 AA.

XX AC AAY01108;

DT 24-MAY-1999 (first entry)

XX HBGF-0.8-P2 peptide fragment obtained by N-terminal sequencing.

XX Heparin-binding growth factor; HBGF; connective tissue growth factor;
XX CTGF; pharmaceutical; wound healing; tissue formation; sclerotic; burn;
XX cell proliferative disorder; atherosclerosis; fibrotic; arthritis; IGF-1;
XX osteoporosis; skeletal disorder; scleroderma; liver cirrhosis; PDGF;
XX insulin-like growth factor; platelet-derived growth factor; TGF-beta;
XX EGF; epidermal growth factor; transforming growth factor beta; BFGF;
XX basic fibroblast growth factor; heparin; growth; placental membrane;
XX endometrial growth; pregnancy; endometrial-trophoblast interaction.

XX Sus scrofa.

XX Key Location/Qualifiers

FT Misc-difference 9 /note= "unspecified"

XX W09907407-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16423.

XX 07-AUG-1997; 97US-0908526.

XX (CHIL-) CHILDRENS HOSPITAL RES FOUND.

XX Brigstock DA, Harding PA;

XX WPI; 1999-167214/14.

XX New substantially pure heparin-binding growth factor polypeptides -
XX useful for affecting wound healing and tissue formation, where
XX antagonists of the polypeptides are useful for, e.g. treating
XX sclerotic or cell proliferative disorders

PS Example 2; Page 27; 53pp; English.

XX The invention relates to a substantially pure heparin-binding growth
CC factor (HBGF) polypeptide (1 kDa) that corresponds to the C-terminal end
CC of a connective tissue growth factor (CTGF) protein. The HBGF
CC polypeptides form pharmaceutical compositions for affecting wound healing
CC and tissue formation. Antagonists of the polypeptides are useful for
CC treating sclerotic or cell proliferative disorders, atherosclerosis or
CC fibrotic conditions. Diseases and conditions modulated by HBGF include
CC arthritis, osteoporosis, and other skeletal disorders, burns. Fibrotic
CC conditions include scleroderma, arthritis and liver cirrhosis. Cells
CC treated are selected from epithelial (especially secretory), muscle
CC (especially smooth or cardiac muscle), connective tissue (especially
CC astroglia, fibroblast, osteoclast, osteoblast or chondrocyte cells) and
CC endothelial (especially endothelial) cells. Each treatment may further
CC comprise the use of growth factors selected from insulin-like growth
CC factor (IGF-1), platelet-derived growth factor (PDGF), epidermal growth
CC factor (EGF), transforming growth factor beta (TGF-beta) or basic
CC fibroblast growth factor (bFGF). The biological effect of HBGF can be
CC modulated using heparin at a concentration of 1-100 mg/ml. HBGF is used
CC for promoting endometrial growth and development of placental membranes
CC and promoting and maintaining pregnancy by facilitating endometrial-
CC trophoblast interaction. The present sequence represents a HBGF peptide
CC fragment obtained by N-terminal sequencing.

XX SQ Sequence 12 AA;

Query Match 41.1%; Score 23; DB 20; Length 12;
Best Local Similarity 42.9%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 3; Mismatches 1;

Qy 2 DNKKAR 8
Db 1 enikgk 7

RESULT 15
AAW89521
ID AAW89521 standard; peptide; 12 AA.

XX AC AAW89521;

XX DT 11-MAR-1999 (first entry)

XX DE Human latent transforming growth factor-beta promoting peptide #6.

XX KW Human; latent transforming growth factor beta; TGF-beta; cancer;
KW atherosclerosis; activity regulator; retinopathy; bone fracture;
KW myocardial infarction; cerebral infarction; hepatic infarction;
KW nephritis; HIV-associated kidney disease; rheumatoid arthritis.

XX OS Homo sapiens.

XX FN W09851704-A1.

XX PD 19-NOV-1998.

XX PF 12-MAY-1998; 98WO-JP02089.

XX PR 12-MAY-1997; 97JP-0120683.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sato Y, Shibata K, Yamasaki M;

XX DR WPI; 1999-059698/05.

XX PT Peptides promoting activation of latent transforming growth factor
PT beta (TGF beta) - for screening potential drugs for treating
PT TGF-associated diseases such as cancer and atherosclerosis

XX PS Claim 6; Page 30; 115pp; Japanese.

XX AAW89516 to AAW89531 represent peptides which promote the activation of
CC latent transforming growth factor beta (TGF-beta). The peptides have
CC the formula R1-A-R2 (1) where R1 = H or (optionally substituted)
CC alkanoyl, arylcarbonyl, heteroarylcarbonyl, alkoxycarbonyl,
CC aryloxycarbonyl or heteroaryloxycarbonyl; R2 = OH, or (optionally
CC substituted) alkoxy or amino; A = a partial sequence from the precursor
CC sequence of TGF-beta, in which up to 5 residues may be added, deleted
CC or substituted, and side-chain amino or carboxy groups may be linked by
CC an amide bond or side-chain mercapto groups may be linked by a
CC disulphide bond. The peptides can be used for the screening of candidate
CC drugs for the treatment and prevention of diseases with which TGF-beta
CC is associated, such as cancer, diabetic complications (e.g.
CC retinopathy), atherosclerosis, bone fractures, myocardial infarction,
CC cerebral infarction, hepatic infarction, nephritis, HIV-associated kidney
CC disease and rheumatoid arthritis.

XX SQ Sequence 12 AA;

Query Match 41.1%; Score 23; DB 20; Length 12;
Best Local Similarity 33.3%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 4; Mismatches 2;

Qy 4 VKKARVQVV 12
Db 2 vkrkrieai 10

RESULT 16
AAB15882
ID AAB15882 standard; Peptide; 12 AA.

XX AC AAB15882;

XX DT 17-JAN-2001 (first entry)

XX DE Human chemokine derived peptide #34.

XX KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception.

XX OS Synthetic.

XX FN W0200042071-A2.

XX PD 20-JUL-2000.

XX PF 12-JAN-2000; 2000WO-US00821.

XX PR 12-JAN-1999; 99US-0229071.

XX PR 17-MAR-1999; 99US-0271192.

XX PR 01-DEC-1999; 99US-0452406.

XX PA (NEOR-) NEORX CORP.

XX PI Grainger DJ, Tatalick LM;

XX DR WPI; 2000-499101/44.

XX PT New peptide 3, amide and heterocyclic compounds and saccharide
PT conjugates used for inhibiting chemokine induced activity and for
PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT growth

XX PS Disclosure; Fig 18; 387pp; English.

XX CC The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines

CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
 CC These chemokine derivatives can be used to treat diseases such as
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models.
 XX
 SQ Sequence 12 AA;

Query Match 41.1%; Score 23; DB 21; Length 12;
 Best Local Similarity 33.3%; Pred. No. 6e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 VKKARVQVV 12
 ||:|::|
 Db 2 vkrkrieai 10

RESULT 17
 AAY78078
 ID AAY78078 standard; Peptide; 12 AA.

AC AAY78078;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:78.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 22; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;

Query Match 41.1%; Score 23; DB 21; Length 12;
 Best Local Similarity 66.7%; Pred. No. 6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 NVKKAR 8
 |::|||
 Db 7 nmrkar 12

RESULT 18

AAR43470

ID AAR43470 standard; peptide; 8 AA.

XX AAR43470;

XX 12-MAY-1994 (first entry)

XX Ro/SSA epitope 315.

XX Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;

KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;

KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';

XX RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.

XX Homo sapiens.

XX WO9321223-A.

XX 28-OCT-1993.

XX 13-APR-1993; 93WO-US03484.

XX 13-APR-1992; 92US-0867819.

XX (OKLA) UNIV OKLAHOMA STATE.

XX Harley JB;

XX WPI; 1993-351658/44.

XX New linear epitope(s) for human auto-antibodies - from the
 PT Ro/SSA, La/SSB and Sm B/B' antigens and ribo:nucleoprotein, used
 PT for diagnosing and treating auto-immune disorders e.g. systemic
 PT lupus erythematosus

XX Claim 1; Page 31; 43pp; English.

XX The sequences given in AAR43391-562 are linear epitopes which are
 CC derived from the 60 kD Ro/SSA peptide, the La/SSB autoantigen,
 CC the 70 kD nuclear ribonucleoprotein (nRNP) and the Sm B/B'
 CC polypeptide. These antigens are common in systemic lupus
 CC erythematosus (SLE) and closely related disorders. The Ro/SSA family
 CC of proteins has been shown to have several molecular forms which are
 CC defined by the molecular weight of the antigen identified. The major
 CC form has a molecular weight of 60 kD and two additional forms have
 CC molecular weights of 52 and 54 kD. La/SSB is also a member of this
 CC group of autoantibodies and binds small RNAs with a pyrimidine
 CC terminus. La/SSB is bound by a third of the anti-Ro/SSA precipitin
 CC positive sera. La/SSB has been shown to be a 46-50 kD monomeric
 CC phosphoprotein which associates with RNA polymerase III transcripts.
 CC Anti-Sm antibodies precipitate snRNPs containing the U1, U2, U4/U6 and
 CC U5 RNA. Anti-Sm antibodies may be directed against one or a
 CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD),
 CC E/F (11 kD doublet) and G (less than 10 kD). These epitopes may be
 CC used for preventing, treating or screening autoimmune disorders,
 CC especially SLE or Sjogrens syndrome (SS). They bind to a human

CC autoantibody and may therefore be used as vaccines.

XX Sequence 8 AA;

Query Match 39.3%; Score 22; DB 14; Length 8;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KkARV 9
||||:
Db 1 Kkari 5

RESULT 19

AAE08182
ID AAE08182 standard; peptide; 8 AA.

XX AC AAE08182;

XX DT 01-NOV-2001 (first entry)

XX DE Peptide #81 from human ribonucleoprotein, 60 kD Ro/SSA.

XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.

XX OS Homo sapiens.

XX PN US6232522-B1.

XX PD 15-MAY-2001.

XX PF 30-NOV-1993; 93US-0160604.

XX PR 31-JAN-1990; 90US-0472947.

XX PR 31-JAN-1991; 91US-0648205.

XX PR 13-APR-1992; 92US-0867819.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Harley JB, James JA, Scofield RH;

XX DR WPI; 2001-335087/35.

XX PT Generating systemic lupus erythematosus animal model by immunizing
PT non-human animal with non-immunoglobulin peptide having amino acid
PT sequence of self-antigen bound by autoantibody population in early
PT stage of disease

XX PS Example 1; Column 16; 63pp; English.

XX CC The patent discloses a specific method of generating an animal model
XX of systemic lupus erythematosus (SLE), comprising immunising a non-
XX human animal with non-immunoglobulin peptide which comprises an
XX epitope immunoreactive with auto-antibody (AAB) from patient with
XX SLE. The epitope includes a region of self-antigen which is bound
XX by AAB population present in early stage in patient with SLE. The
XX method is used for generating an animal model of SLE. It is useful
XX for screening therapeutics effective in treating autoimmune disorders.
XX It is useful as a component in a diagnostic assay, as a therapeutic
XX (vaccine to block the AABs produced, by eliciting immune response),
XX and in research on the possible causes of the autoimmune diseases.
XX The method is used to interrupt the course of an autoimmune response,
XX once autoimmunity against the autoantigen is established. The amino
XX acid sequences are used to make agents for neutralising circulating
XX antibodies or immobilised on substrates in extracorporeal devices for
XX specific removal of AABs. The reagents identified by using the method
XX are useful in manufacturing and testing autoantigens. The method is
XX useful as models for screening of compounds which induce autoimmunity,
XX inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX in diagnosis of autoimmunity and as therapeutics for the treatment of
XX autoimmune disorders. The present sequence is a peptide from human ribo-

CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX of the invention.

SQ Sequence 8 AA;

Query Match 39.3%; Score 22; DB 22; Length 8;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KkARV 9
||||:
Db 1 Kkari 5

RESULT 20

AAE75015
ID AAR75015 standard; peptide; 9 AA.

XX AC AAR75015;

XX DT 16-JAN-1996 (first entry)

XX DE Deletion mutant delta 175-179 of human p55 TNF-R spacer region.

XX KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA; spacer region.

XX OS Synthetic.

XX PN AU9475742-A.

XX PD 04-MAY-1995.

XX PF 11-OCT-1994; 94AU-0075742.

XX PR 12-OCT-1993; 93IL-0107268.

XX PA (VEDA) VEDA RES & DEV CO LTD.

XX PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;

XX DR WPI; 1995-194342/26.

XX PT New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF- receptor, useful for
PT antagonising deleterious effects of TNF.

XX PS Example 2; Fig 5; 40pp; English.

XX CC The sequences represented in AAR75013-25 are fragments of deletion
XX mutants of the spacer region of human p55 tumour necrosis factor (TNF-R),
XX shown in AAR75012. Expression of this receptor is regulated by shedding
XX of the extracellular receptor fragment. The p55 TNF-R can be shed in
XX response to different inducing agents, e.g. phorbol myristate acetate
XX (PMA), depending on cell type. The only region of the receptor whose
XX structure affects the shedding response is the spacer region in the
XX extracellular domain. This region is located close to a site of cleavage
XX of the molecule, and links the Cys rich module to the transmembranal
XX domain. The sequences shown in AAR75026-47 are fragments of replacement
XX mutations of the spacer region. These mutations were introduced in order
XX to create an inhibitor of a protease that is capable of cleaving the
XX soluble TNF-R from the cell bound TNF-R. The relevant fragments of the
XX successful inhibitors can be seen in AAR75017-9, AAR75025, AAR75033-5 and
XX AAR75042-3. The protease inhibitors can be used for enhancing TNF
XX function.

XX SQ Sequence 9 AA;

Query Match 39.3%; Score 22; DB 16; Length 9;
Best Local Similarity 55.6%; Pred. No. 6.4e+05;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDNVKKARV 9
I:III I
Db 1 IENVKgttv 9

Search completed: July 8, 2002, 11:42:58
Job time: 230 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:47:54 ; Search time 14.12 Seconds
(without alignments)
217.766 Million cell updates/sec

Title: US-09-461-061a-4
Perfect score: 161
Sequence: 1 TLTHTTITKLNAENNAFFKIDNVKKARVQVV 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 6873

Minimum DB seq length: 0
Maximum DB seq length: 32

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	21.1	31	2 G70123	hypothetical prote
2	33.5	20.8	20	2 D41299	T-cell receptor al
3	33	20.5	25	2 S03500	T-cell receptor ga
4	31	19.3	30	2 S77821	hypothetical prote
5	30.5	18.9	32	2 S32971	dodecandrin - endo
6	30	18.6	25	2 H64710	hypothetical prote
7	29	18.0	20	2 A53875	creatine kinase (E
8	29	18.0	26	2 S16336	beta-conglycinin b
9	28.5	17.7	29	2 I50214	protein-tyrosine-p
10	28	17.4	16	2 PH1580	Ig H chain V-D-J r
11	28	17.4	30	2 J50645	diuretic hormone I
12	28	17.4	30	2 P89864	hypothetical prote
13	28	17.4	32	2 A95108	hypothetical prote
14	27.5	17.1	29	2 P00762	NADH dehydrogenase
15	27	16.8	14	2 S62374	alpha-1-antichymot
16	27	16.8	18	2 S58855	botulinum neurotox
17	27	16.8	24	2 C85846	unknown protein en
18	27	16.8	25	2 B47689	flagellar core pro
19	27	16.8	28	2 I40034	trpE protein - Bac
20	27	16.8	28	2 PL0005	pepsin A (EC 3.4.2
21	27	16.8	31	2 E87331	hypothetical prote
22	27	16.8	32	2 C49480	major immunophilin
23	27	16.8	32	2 A44906	L1 protein - human
24	26.5	16.5	31	2 E95151	hypothetical prote
25	26.5	16.5	32	2 F81385	hypothetical prote
26	26	16.1	16	2 I52226	aldehyde dehydroge
27	26	16.1	18	2 A42576	steroid receptor c
28	26	16.1	24	2 I61491	seed protein ws-9
29	26	16.1	25	2 S39391	calpain II heavy c

30 26 16.1 28 2 S77854
31 26 16.1 28 2 S11618
32 26 16.1 28 2 S49924
33 26 16.1 29 2 A45474
34 26 16.1 31 2 T44925
35 26 16.1 31 2 A64630
36 25 15.5 10 2 PH0807
37 25 15.5 15 2 A56970
38 25 15.5 15 2 PH1610
39 25 15.5 21 2 A60225
40 25 15.5 22 2 S12391
41 25 15.5 24 2 C47689
42 25 15.5 28 1 G98PSV
43 25 15.5 30 2 S27306
44 25 15.5 31 2 A24730
45 25 15.5 31 2 S78738

ALIGNMENTS

RESULT 1

G70123
hypothetical protein BB0191 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: G70123
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943
A:Accession: G70123
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <KLE>
A:Cross-references: GB:AE001129; GB:AE000783; NID:g2688071; PIDN:AAC66583.1; PID:g268
A:Experimental source: strain B31

Query Match 21.1%; Score 34; DB 2; Length 31;
Best Local Similarity 41.7%; Pred. No. 4.6e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 20 KIDNVKKARVQV 31

Db 7 KINNIDKTNIQI 18

RESULT 2

D41299
T-cell receptor alpha chain precursor (26.1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C:Accession: D41299
R:Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A:Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheum
A:Reference number: A41299; MUID:92020887
A:Accession: D41299
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <UEM>
A:Cross-references: GB:S57442; NID:g236324; PIDN:AAB19959.1; PID:g236325
C:Keywords: T-cell receptor

Query Match 20.8%; Score 33.5; DB 2; Length 20;
Best Local Similarity 47.4%; Pred. No. 3.5e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 TLTHTTITKLNAENNAATFYF 19
: ||| || || : : ||
Db 1 SLTH-ITALNKKVDSAVYF 18

RESULT 3

S03500
T-cell receptor gamma chain V region (FT6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 30-May-1997
C:Accession: S03500
R:Heilig, J.S.; Tonegawa, S.
Nature 322, 836-840, 1986
A:Title: Diversity of murine gamma genes and expression in fetal and adult T lymphocytes
A:Reference number: S03498; MUID:86311315
A:Accession: S03500
A:Molecule type: mRNA
A:Residues: 1-25 <HEI>
A:Cross-references: EMBL:X04396
A:Note: The authors translated the codon AAG for residue 1 as Leu and GCC for residue 24
A:Note: This sequence was determined from the nonfunctional differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 20.5%; Score 33; DB 2; Length 25;

Best Local Similarity 46.2%; Pred. No. 5e+02;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 12 ENNAATFYFKIDNV 24

: : : ||| |||

Db 1 KDDGTFYLIINN 13

RESULT 4

S77821
Hypothetical protein MC318 - Mycoplasma capricolum (fragment)
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 14-Nov-1997 #text_change 07-Dec-1999
C:Accession: S77821; S46915
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A:Reference number: S77739; MUID:96059641
A:Accession: S77821
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-30 <BOR>
A:Cross-references: EMBL:X23233
A:Experimental source: ATCC 27343
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3

Query Match 19.3%; Score 31; DB 2; Length 30;

Best Local Similarity 26.3%; Pred. No. 1.1e+03;

Matches 5; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 10 NAENNAATFYFKIDNVKKAR 28

: : : ||| ||| : :

Db 4 NSRQXSREYHVIENLXKK 22

RESULT 5

S32971
dodecandrin - endod pokeweed (fragment)
C:Species: Phytolacca dodecandra (endod pokeweed)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: S32971
R:Ready, M.P.; Adams, R.P.; Robertus, J.D.
Biochim. Biophys. Acta 791, 314-319, 1984
A:Title: Dodecandrin, a new ribosome-inhibiting protein from Phytolacca dodecandra.

A:Reference number: S32971; MUID:85097746

A:Accession: S32971

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-32 <REA>

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

Query Match 18.9%; Score 30.5; DB 2; Length 32;

Best Local Similarity 28.0%; Pred. No. 1.4e+03;

Matches 7; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

Qy 1 TLTHTTITKLNAENNAATFYFKIDNVK 25

: : : ||| ||| : :

Db 3 TIIYVGSSTTISNYATF--MDNLR 24

RESULT 6

H64710

hypothetical protein HP1528 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: H64710

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcke

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467

A:Accession: H64710

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-25 <TOM>

A:Cross-references: GB:AE000651; GB:AE000511; NID:92314708; PIDN:AAD08577.1; PID:9231

Query Match

18.6%; Score 30; DB 2; Length 25;

Best Local Similarity 44.4%; Pred. No. 1.3e+03;

Matches 8; Conservative 6; Mismatches 2; Indels 2; Gaps 2;

Qy 17 FYFK-ID-NVKKARVQVV 32

: : : ||| ||| ||| :

Db 5 FYFRFLDYSLKKGLVKVI 22

RESULT 7

A53875

creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)

C:Species: Oncorhynchus kisutch (coho salmon)

C:Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C:Accession: A53875

R:White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.

J. Protein Chem. 11, 489-494, 1992

A:Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB

A:Reference number: A53875; MUID:93080727

A:Accession: A53875

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-20 <WHI>

A:Experimental source: Brockmann body, principal islet

A:Note: sequence extracted from NCBI backbone (NCBIP:120599)

C:Superfamily: creatine kinase; creatine kinase repeat homology

C:Keywords: phosphotransferase

Query Match

18.0%; Score 29; DB 2; Length 20;

Best Local Similarity 38.5%; Pred. No. 1.4e+03;

Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 10 NAENNAATFYFKID 22

: : ||| ||| :

Db 4 NTHNFKLNFKVE 16

C;Keywords: immunoglobulin

Query Match 17.4%; Score 28; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 17 FYFKIDN 23
||: ||
Db 10 FYAMDN 16

RESULT 11
JS0645
diuretic hormone II - tobacco hornworm
N;Alternate names: diuretic peptide II
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Apr-2001
C;Accession: JS0645
R;Blackburn, M.B.; Kingan, T.G.; Bodnar, W.; Shabanowitz, J.; Hunt, D.F.; Kempe, T.;
Biochem. Biophys. Res. Commun. 181, 927-932, 1991
A;Title: Isolation and identification of a new diuretic peptide from the tobacco horn
A;Reference number: JS0645; MUID:92109782
A;Accession: JS0645
A;Molecule type: protein
A;Residues: 1-30 <BLA>
C;Comment: This hormone is a factor which increases the rate of fluid excretion in th
C;Keywords: amidated carboxyl end
F;30/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 17.4%; Score 28; DB 2; Length 30;
Best Local Similarity 30.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTHITITKLNAENNAEYFKI 21
| | : | : | | : |
Db 11 LQHYMEKVAONNRNRLNRV 30

RESULT 12
F89864
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89864
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89864
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <KUR>
A;Cross-references: GB:BA000018; PID:g13700777; PIDN:BA042073.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA5024

Query Match 17.4%; Score 28; DB 2; Length 30;
Best Local Similarity 46.2%; Pred. No. 2.8e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNA 15
| | : | : | | : |
Db 15 TORISKRNSTGNA 27

RESULT 13
A95108

Query Match 18.0%; Score 29; DB 2; Length 26;
Best Local Similarity 31.2%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 8 KLNNAENNAEYFKIDN 23
| : | | : |
Db 2 KVEDENPFILRSSN 17

RESULT 9
I50214
protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C;Accession: I50214
R;Stoker, A.W.
Mech. Dev. 46, 201-217, 1994
A;Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase an
A;Reference number: I50212; MUID:95001563
A;Accession: I50214
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-29 <STO>
A;Cross-references: GB:L32782; NID:g485750; PIDN:AAA64462.1; PID:g485751
C;Gene: CRYPalpha3
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 17.7%; Score 28.5; DB 2; Length 29;
Best Local Similarity 31.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 12 ENNATFEYFKIDNVKK-ARVQVV 32
||| : : : |||
Db 8 ENNSTIVVMTKLRLMGKRVSL 29

RESULT 10
PH1580
Ig H chain V-D-J region (wild-type clone 3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1580
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609
A;Accession: PH1580
A;Molecule type: DNA
A;Residues: 1-16 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 17.4%; Score 28; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 17 FYFKIDN 23
||: ||
Db 10 FYAMDN 16

RESULT 11
JS0645
diuretic hormone II - tobacco hornworm
N;Alternate names: diuretic peptide II
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Apr-2001
C;Accession: JS0645
R;Blackburn, M.B.; Kingan, T.G.; Bodnar, W.; Shabanowitz, J.; Hunt, D.F.; Kempe, T.;
Biochem. Biophys. Res. Commun. 181, 927-932, 1991
A;Title: Isolation and identification of a new diuretic peptide from the tobacco horn
A;Reference number: JS0645; MUID:92109782
A;Accession: JS0645
A;Molecule type: protein
A;Residues: 1-30 <BLA>
C;Comment: This hormone is a factor which increases the rate of fluid excretion in th
C;Keywords: amidated carboxyl end
F;30/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 17.4%; Score 28; DB 2; Length 30;
Best Local Similarity 30.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTHITITKLNAENNAEYFKI 21
| | : | : | | : |
Db 11 LQHYMEKVAONNRNRLNRV 30

RESULT 12
F89864
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89864
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89864
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <KUR>
A;Cross-references: GB:BA000018; PID:g13700777; PIDN:BA042073.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA5024

Query Match 17.4%; Score 28; DB 2; Length 30;
Best Local Similarity 46.2%; Pred. No. 2.8e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNA 15
| | : | : | | : |
Db 15 TORISKRNSTGNA 27

RESULT 13
A95108

hypothetical protein SP0934 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: A95108
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A.:Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-32 <KUR>
A:Cross-references: GB:AF005672; PIDN:AAK75058.1; PID:g14972409; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0934

Query Match 17.4%; Score 28; DB 2; Length 32;
Best Local Similarity 46.2%; Pred. No. 3e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 14 NATFFFKIDNVKK 26
| | : : | | |
Db 19 NPYFFDRIEVKK 31
| | : : | | |

RESULT 14
PQ0782
NADH dehydrogenase (EC 1.6.99.3) 31K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 31K chain; NADH-ubiquinone reductase 31K chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: PQ0782
R:Letierme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:
A:Reference number: PQ0775; MUID:94151437
A:Accession: PQ0782
A:Molecule type: protein
A:Residues: 1-29 <LET>
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 17.1%; Score 27.5; DB 2; Length 29;
Best Local Similarity 27.6%; Pred. No. 3.2e+03;
Matches 8; Conservative 3; Mismatches 13; Indels 5; Gaps 1;

Qy 6 ITKLN----AENNATFFFKIDNVKKARV 29
: | | | : : : | | |
Db 1 VTALNHLSDPNPNLLHFFHNAKKEV 29
: | | | : : : | | |

RESULT 15
S62374
alpha-1-antichymotrypsin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
C:Accession: S62374
R:Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
Eur. J. Biochem. 235, 821-827, 1996
A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia
A:Reference number: S62374; MUID:96184564
A:Accession: S62374
A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-14 <TSU>

Query Match 16.8%; Score 27; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 14 NATFFFKIDNVKKA 27
| | | : | | |
Db 1 NIFFMSKVTNPKQA 14
| | | : | | |

RESULT 16
S58855
botulinum neurotoxin type B nontoxic-nonhemagglutinin component - Clostridium botulin
N:Alternate names: NTNH protein
C:Species: Clostridium botulinum
A:Variety: strain Eklund 17B
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 15-Oct-1999
C:Accession: S58855
R:East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A:Title: Cloning and sequencing of a hemagglutinin component of the botulinum neuroto
A:Reference number: S58855
A:Accession: S58855
A:Molecule type: DNA
A:Residues: 1-18 <EAS>
A:Cross-references: EMBL:X79103; NID:9870932; PIDN:CAA55712.1; PID:9870933
A:Experimental source: strain Eklund 17B
C:Keywords: neurotoxin

Query Match 16.8%; Score 27; DB 2; Length 18;
Best Local Similarity 29.4%; Pred. No. 2.3e+03;
Matches 5; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 9 LNAENNATFFFKIDNVK 25
: | | : : | | |
Db 1 MNINDNLSINSPVDNKK 17
| | | : | | |

RESULT 17
C85846
unknown protein encoded within prophage Cp-933V [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85846
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-24 <STO>
A:Cross-references: GB:AF005174; NID:g12516398; PIDN:AAG57231.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3347

Query Match 16.8%; Score 27; DB 2; Length 24;
Best Local Similarity 25.0%; Pred. No. 3.1e+03;
Matches 5; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 4 HTITKLNNAENNATFFFKIDN 23
| | : : | | : : |
Db 4 HCCAELMSDPNNSMYEEDD 23
| | : : | | : : |

RESULT 18

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:49:54 ; Search time 10.26 Seconds
(without alignments)
120.763 Million cell updates/sec

Title: US-09-461-061A-4
Perfect score: 161
Sequence: 1 TLHTITKLNAENNATYFKIDNVKARQVQV 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 2064

Minimum DB seq length: 0
Maximum DB seq length: 32

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	21.1	24	1 DNAJ_STRAG	P95694 streptococ
2	34	21.1	31	1 Y191_BORBU	O51209 borrelia bu
3	28.5	17.7	20	1 CHP_THICU	P80486 thiobacillu
4	28	17.4	30	1 DIU2_HYLLI	P82015 hyles linea
5	28	17.4	30	1 DIU2_WANSE	P24858 manduca sex
6	27	16.8	25	1 FLB1_TREHY	P80158 treponema h
7	25	15.5	15	1 MM01_RAT	P81563 rattus norv
8	25	15.5	15	1 TRPB_KLEAE	P14552 klebsiella
9	25	15.5	20	1 FLA2_SPIAU	P21985 spirochaeta
10	25	15.5	27	1 FLA1_SPIAU	P21984 spirochaeta
11	25	15.5	28	1 VG9_SPV4	P11341 spiroplasma
12	25	15.5	31	1 COM4_NEUCR	P06809 neurospora
13	24.5	15.2	18	1 FWF1_ECOLI	P20860 escherichia
14	24.5	15.2	29	1 RS7_METTE	O93639 methanosarc
15	24	14.9	15	1 NTS1_ANAVA	O44507 anabaena va
16	24	14.9	21	1 FA71_TETPY	P81424 tetrahymena
17	24	14.9	21	1 LPT1_ECOLI	P03059 escherichia
18	24	14.9	24	1 LPTN_ECOLI	P09408 escherichia
19	24	14.9	26	1 PUTA_KLEPN	P23725 klebsiella
20	24	14.9	30	1 AMPT_BACST	P00728 bacillus st
21	24	14.9	31	1 CEC1_PIG	P14661 sus scrofa
22	23.5	14.6	30	1 AL21_HORSE	P81216 equus caball
23	23.5	14.6	30	1 RPS_MOMCO	P20655 momordica c
24	23.5	14.6	32	1 DBH_SYNY1	P02343 synechocyst
25	23	14.3	19	1 FLA3_SPIAU	P21986 spirochaeta
26	23	14.3	20	1 LPP2_HUMAN	P56642 homo sapien
27	23	14.3	21	1 CXGT_CONTU	P17684 conus tulip
28	23	14.3	27	1 FLA4_SPIAU	P21987 spirochaeta
29	23	14.3	31	1 HEM2_PHAGO	P27687 phascoglossi
30	23	14.3	32	1 YCPG_MASLA	P29735 mastigoclad
31	22	13.7	16	1 ALI1_CALVO	P41839 calliphora
32	22	13.7	24	1 HEMU_LINRE	P23544 lingula ree
33	22	13.7	26	1 YFHA_KLEPN	P21710 klebsiella

ALIGNMENTS

RESULT 1					
DNAJ_STRAG					
ID	DNAJ_STRAG	STANDARD;	PRT;	24 AA.	
AC	P95694;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Chaperone protein dnaJ (Fragment).				
GN	DNAJ.				
OS	Streptococcus agalactiae.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1311;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Rioux C.R., Martin D., Hamel J., Brodeur B.R.;				
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,				
CC	THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).				
CC	-!- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE DNAJ FAMILY.				
CC	-!- SIMILARITY: CONTAINS 1 J DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
EMBL; U72719;	AA839220.1;				
DR	InterPro; IPR001305; DnaJ_CXXCXGKG.				
DR	InterPro; IPR001623; DnaJ_N.				
DR	PROSITE; PS00636; DnaJ_1; PARTIAL.				
DR	PROSITE; PS0076; DnaJ_2; PARTIAL.				
DR	PROSITE; PS00637; DnaJ_CXXCXGKG; PARTIAL.				
KW	Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding.				
FT	DOMAIN 3 >24				
FT	NON_TER 24				
FT	J-DOMAIN				
SQ	SEQUENCE 24 AA; 2760 MW; 342AB656E00913FC CRC64;				

Query Match 21.1%; Score 34; DB 1; Length 24;
Best Local Similarity 34.8%; Pred. No. 83;
Matches 8; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 13 NNATFYFKI-----DNVKA 27

DB 2 NNTFYDLRGVSKDASQDEIKKA 24

RESULT 2

Y191_BORBU STANDARD; PRT; 31 AA.
ID Y191_BORBU

```
AC O51209;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0191.
GN BB0191.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Castjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
RA Peterson J., Kierlavage A.R., Quackenbush J., Salzberg S., Johnson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CR EMBL: AE001129; AAC66583.1;
DR TIGR: BB0191;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 31 AA; 3583 MW; 4DDA4AF26162455E CRC64;

Query Match 21.1%; Score 34; DB 1; Length 31;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 20 KIDNVKKARVQV 31
Db ||:|:|:|:|:
7 KINIDKNTIQI 18

RESULT 3
CHP_THICU
ID CHP_THICU STANDARD; PRT; 20 AA.
AC P80486;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemoterotroph-specific protein (Fragment).
OS Thioabaillus cuprinus.
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOHETEROTROPHICALLY.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2167 MW; E5BAEC1BA3238A0A CRC64;

Query Match 17.7%; Score 28.5; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
```

```
QY 2 LHTHTITKLNAENNATFYFKID 22
Db ||:|:|:|:|:|:|:|:|:|:
2 LHYTGTVINVQ---TFAAKPD 19

RESULT 4
DIU2_HYLLI
ID DIU2_HYLLI STANDARD; PRT; 30 AA.
AC P82015;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diuretic hormone 2 (DH-2) (Diuretic peptide 2) (DP-2) (DH(30)).
OS Hyles lineata (Whitelined sphinx moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Macroglossinae; Hyles.
OX NCBI_TaxID=103890;
RN [1]
RP SEQUENCE, ACTIVITY, AND AMIDATION.
RC TISSUE=Head;
RX MEDLINE=20161578; PubMed=10696588;
RA Furuya K., Harper M.A., Schegg K.M., Shooley D.A.;
RT "Isolation and characterization of CFR-related diuretic hormones from
RT the whitelined sphinx moth Hyles lineata."
RL Insect Biochem. Mol. Biol. 20:127-133(2000).
CC -!- FUNCTION: REGULATION OF FLUID SECRETION. MAY STIMULATE PRIMARY
CC URINE SECRETION BY MALPIGHIAN TUBULES AND CAUSES A DOSE-DEPENDENT
CC STIMULATION OF CAMP LEVELS IN THE TUBULES.
CC -!- MASS SPECTROMETRY: MW=3574; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
CR InterPro: IPR000187; CRF.
DR Pfam: PF00473; CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; FALSE_NEG.
KW Hormone; Amidation.
FT MOD_RES 30
SQ SEQUENCE 30 AA; 3575 MW; 5C2D6BD2DD8BFC67 CRC64;

Query Match 17.4%; Score 28; DB 1; Length 30;
Best Local Similarity 30.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 LHTHTITKLNAENNATFYFKI 21
Db ||:|:|:|:|:|:|:|:|:|:
11 LQHYMEKVAQNNRNLNRV 30

RESULT 5
DIU2_MANSE
ID DIU2_MANSE STANDARD; PRT; 30 AA.
AC P24858;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diuretic hormone 2 (DH-2) (Diuretic peptide 2) (DP-2) (DPII).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92109782; PubMed=1764106;
RA Blackburn M.B., Kingan T.G., Bodnar W., Shabanowitz J., Hunt D.F.,
RA Kempe T., Wagner R.M., Raina A.K., Schnee M.E., Ma M.C.;
RT "Isolation and identification of a new diuretic peptide from the
RT tobacco hornworm, Manduca sexta."
RL Biochem. Biophys. Res. Commun. 181:927-932(1991).
```

```
CC -|- FUNCTION: REGULATION OF FLUID SECRETION.
CC -|- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UTENSIN I FAMILY OF PEPTIDES.
DR PIR; JS0645; JS0645.
DR InterPro; IPR000187; CRF.
DR Pfam; PF00473; CRF; 1.
DR SMART; SM00039; CRF; 1.
DR PROSITE; PS00511; CRF; FALSE_NEG.
KW Hormone; Amidation.
FT MOD_RES 30 30 AMIDATION.
SQ SEQUENCE 30 AA; 3561 MW; 5C2D6BD2D08A2717 CRC64;

Query Match 17.48; Score 28; DB 1; Length 30;
Best Local Similarity 30.08; Pred. No. 7.4e+02;
Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTHTTIKLNAENNATFYFKI 21
Db 11 LQHYMEKVAQNNRFLNRV 30

RESULT 6
FLB1_TREHY STANDARD; PRT; 25 AA.
ID FLB1_TREHY STANDARD; PRT; 25 AA.
AC P80158;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament core protein flab1 (37 kDa core protein)
DE (Fragment).
DE FLAB1
GN FLAB1
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -|- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.
CC -|- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
CC FLAB3 (32 kDa).
CC -|- SUBCELLULAR LOCATION: Periplasmic flagellum.
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
DR PIR; B47689; B47689.
KW Flagella; Periplasmic.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2915 MW; BBB699593CD398B6 CRC64;

Query Match 16.88; Score 27; DB 1; Length 25;
Best Local Similarity 28.08; Pred. No. 8.3e+02;
Matches 7; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

Oy 2 LTHTTIKLNAENNATFYFKIDNVKK 26
Db 3 INNINISAINAQR--TLKFRQVDLKK 25

RESULT 7
MM01_RAT STANDARD; PRT; 15 AA.
ID MM01_RAT STANDARD; PRT; 15 AA.
AC P81563;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

```
DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
DE (MMP-1) (fibroblast collagenase) (Myocardial collagenase) (Fragment).
GN MMP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=96201136; PubMed=8605638;
RA Tyagi S.C., Cleutjens J.P.M.;
RT "Myocardial collagenase: purification and structural
RT characterization.";
RL Can. J. Cardiol. 12:165-171(1996).
CC -|- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY
CC PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR
CC MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.
CC -|- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where PI' is a
CC hydrophobic residue.
CC -|- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -|- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -|- PTM: THE N-TERMINAL IS BLOCKED.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;
KW Extracellular matrix.
FT NON_TER 1 15
SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;

Query Match 15.58; Score 25; DB 1; Length 15;
Best Local Similarity 55.68; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 9 LNAENNATF 17
Db 3 LKSEKNADF 11

RESULT 8
TRPB_KLEAE STANDARD; PRT; 19 AA.
ID TRPB_KLEAE STANDARD; PRT; 19 AA.
AC P14552;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tryptophan synthase beta chain (EC 4.2.1.20) (Fragment).
GN TRPB.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81199002; PubMed=6262736;
RA Nicholas B.P., Blumenberg M., Yanofsky C.;
RT "Comparison of the nucleoside sequence of trpA and sequences
RT immediately beyond the trp operon of Klebsiella aerogenes. Salmonella
RT typhimurium and Escherichia coli.";
RL Nucleic Acids Res. 9:1743-1755(1981).
CC -|- FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR THE SYNTHESIS
CC OF L-TRYPTOPHAN FROM INDOLE AND L-SERINE.
CC -|- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
```

CC -!- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRPB FAMILY.
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; V00630; CRA23901.1; -;
DR EMBL; J01738; AAA25144.1; -;

DR HSSP; P00933; 2TYS.

DR InterPro; IPR000593; TYP_synth_beta.

DR PROSITE; PS00168; TRP_SYNTHASE_BETA; PARTIAL.

KW Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.

FT NON_TER 1

SQ SEQUENCE 19 AA; 2183 MW; 82864627BF574E2C CRC64;

Query Match 15.5%; Score 25; DB 1; Length 19;

Best Local Similarity 30.8%; Pred. No. 1.2e+03;

Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 19 FKIDNVKRVQV 31

I : : : I I I : :

DB 7 FTVHDLKARGEI 19

RESULT 9

FLA2_SPIAU

ID FLA2_SPIAU STANDARD; PRT; 20 AA.

AC P21985;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Flagellar filament 33 kDa core protein (Minor) (Fragment).

OS Spirochaeta aurantia.

OC Bacteria; Spirochaetales; Spirochaetaceae; Spirochaeta.

OX NCBI_TaxID=147;

RN [1]

RP SEQUENCE.

RC STRAIN=M1;

RX MEDLINE=91123217; PubMed=1991729;

RA Parales J. Jr., Greenberg E.P.;

RT "N-terminal amino acid sequences and amino acid compositions of the

RT Spirochaeta aurantia flagellar filament polypeptides.";

RL J. Bacteriol. 173:1357-1359(1991).

CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.

CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF

CC FIVE ANTIGENICALLY RELATED POLYPEPTIDES.

CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.

CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.

KW Flagella; Periplasmic.

FT NON_TER 20

SQ SEQUENCE 20 AA; 2166 MW; FFCB66276472BF5B CRC64;

Query Match

Best Local Similarity 15.5%; Score 25; DB 1; Length 20;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LTHITTKLNAE 12

: | : : : | :

DB 3 INHNMSAINAQ 13

RESULT 10

FLA1_SPIAU

ID FLA1_SPIAU STANDARD; PRT; 27 AA.
AC P21984;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament 34 kDa core protein (Major) (Fragment).
OS Spirochaeta aurantia.
OC Bacteria; Spirochaetales; Spirochaetaceae; Spirochaeta.
OX NCBI_TaxID=147;
RN [1]
RP SEQUENCE.
RC STRAIN=M1;
RX MEDLINE=91123217; PubMed=1991729;
RA Parales J. Jr., Greenberg E.P.;

RT "N-terminal amino acid sequences and amino acid compositions of the

RT Spirochaeta aurantia flagellar filament polypeptides.";

RL J. Bacteriol. 173:1357-1359(1991).

CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.

CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF

CC FIVE ANTIGENICALLY RELATED POLYPEPTIDES.

CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.

CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.

KW Flagella; Periplasmic.

FT NON_TER 27

SQ SEQUENCE 27 AA; 2942 MW; CEB9060FA32682BF CRC64;

Query Match

Best Local Similarity 15.5%; Score 25; DB 1; Length 27;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LTHITTKLNAE 12

: | : : : | :

DB 3 INHNMSAINAQ 13

RESULT 11

VG9_SPV4

ID VG9_SPV4 STANDARD; PRT; 28 AA.

AC P11341;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 01-JUL-1989 (Rel. 11, Last annotation update)

DE Gene 9 protein.

GN 9.

OS Spiroplasma virus 4 (Spv4).

OC Viruses; ssDNA viruses; Microviridae; Spiromicrovirus.

OX NCBI_TaxID=10855;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88032809; PubMed=2822658;

RA Renaudin J., Pascarel M.-C., Bove J.-M.;

RT "Spiroplasma virus 4: nucleotide sequence of the viral DNA,

RT regulatory signals, and proposed genome organization.";

RL J. Bacteriol. 169:4950-4961(1987).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC EMBL; M17988; -; NOT_ANNOTATED_CDS.

DR PIR; B29825; G9BPSV.

SQ SEQUENCE 28 AA; 3776 MW; 9916C3C9C3B9FD1D CRC64;

Query Match

Best Local Similarity 15.5%; Score 25; DB 1; Length 28;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;


```
QY 19 FKIDNVKKARVQ 30
  || | | | |
Db 6 FKTSRVVKKHRV 17

RESULT 12
COXA_NEUCR
ID COX4_NEUCR STANDARD; PRT; 31 AA.
AC P06809;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide IV, mitochondrial precursor
DE (EC 1.9.3.1) (Fragment).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariales; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3001085;
RX MEDLINE=86085927; PubMed=3001085;
RA Sachs M.S., David M., Werner S., Rajbandary U.L.;
RT "Nuclear genes for cytochrome c oxidase subunits of Neurospora
RT crassa. Isolation and characterization of cDNA clones for subunits
RT IV, V, VI, and possibly VII."
RL J. Biol. Chem. 261:869-873(1986).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE Vb FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M12116; AAA33574.1; -
RW PIR; A25629; A25629.
KW Oxidoreductase; Mitochondrion; Inner membrane; Transit peptide.
FT NON_TER 1 16 MITOCHONDRION.
FT TRANSIT <1 16
FT CHAIN 17 >31 CYTOCHROME C OXIDASE POLYPEPTIDE IV.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3397 MW; 069F5D5510300362 CRC64;

Query Match 15.5%; Score 25; DB 1; Length 31;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLTHITIKLNAE 12
  :: | : |||
Db 8 SIATTVVRCNAE 19

RESULT 13
FMF1_ECOLI
ID FMF1_ECOLI STANDARD; PRT; 18 AA.
AC P20860;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE F7-1 fimbrial protein (F7-1 pilin) (P adhesin) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.

Query Match 15.2%; Score 24.5; DB 1; Length 29;
Best Local Similarity 39.1%; Pred. No. 2.2e+03;
Matches 9; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

RX MEDLINE=89079313; PubMed=2562836;
RA Hoshuetzky H., Lottspeich F., Jann K.;
RT "Isolation and characterization of the alpha-galactosyl-1,4-beta-
RT galactosyl-specific adhesin (P adhesin) from fimbriated Escherichia
RT coli."
RL Infect. Immun. 57:76-81(1989).
CC -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -!- MISCELLANEOUS: THIS IS A ALPHA-GALACTOSYL-1,4-BETA-GALACTOSYL-SPE
CC CJFIC ADHESIN.
DR PIR; A30541; A30541.
KW Fimbria.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1956 MW; E9A44CDA6E2886B5 CRC64;

Query Match 15.2%; Score 24.5; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 13 NNATFYFKIDNV 24
  || | | : ||
Db 2 NNIVFY-SLGNV 12

RESULT 14
RS7_METTE
ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S7P (Fragment).
GN RP57P OR S7.
OS Methanosarcina thermophila.
OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
OC Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1825 / TW-1;
RX MEDLINE=99059471; PubMed=9845338;
RA Thomas T., Cavicchioli R.;
RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
RT thermophilic methanogens."
RL FEBS Lett. 439:281-287(1998).
CC -!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
CC 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF026165; AAC79199.1; -
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 15.2%; Score 24.5; DB 1; Length 29;
Best Local Similarity 39.1%; Pred. No. 2.2e+03;
Matches 9; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
```

```
QY 9 LNAENNATFYFKIDNVKARQV 31
   : | | | | | | | | | | : |
Db 3 IGAANRDTKFSFI-NRKDAKERV 24

RESULT 15
NISL_ANAVA
ID NISL_ANAVA STANDARD; PRT; 15 AA.
AC Q44507;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteine desulfurase 1 (EC 4.4.1.-) (Nitrogenase metallocusters
DE biosynthesis protein nifS1) (Fragment).
GN NIFS1 OR NIFS.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7937 / ATCC 29413;
RA Monnerlahn U., Boehme H.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP EXPRESSION PATTERN.
RC STRAIN=PCC 7937 / ATCC 29413;
RX MEDLINE=96016168; PubMed=7568132;
RA Thiel T., Lyons E.M., Erker J.C., Ernst A.;
RT "A second nitrogenase in vegetative cells of a heterocyst-forming
cyanobacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
CC -!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE
CC BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE
CC INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
CC SIMILARITY).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- MISCELLANEOUS: BELONGS TO THE NIF1 GENE CLUSTER WHICH IS EXPRESSED
CC IN HETEROCYSTS UNDER ANAEROBIC AND AEROBIC CONDITIONS.
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
CC -----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
EMBL; X69898; CAA49523.1; -
DR InterPro: IPR000192; AminoTransf_class.V
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; PARTIAL.
FW Nitrogen fixation; Lyase; Pyridoxal phosphate.
KT NON_TER 15
SQ SEQUENCE 15 AA; 1684 MW; 08B8F106DE65547D CRC64;

Query Match 14.9%; Score 24; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 12 ENNATFYFKID 22
   : | | | | | | |
Db 7 DNNAT--TKVD 15

RESULT 16
FA7L_TETPY
ID FA7L_TETPY STANDARD; PRT; 21 AA.
AC P81424;
DT 15-DEC-1998 (Rel. 37, Created)
```

```
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 71 kDa F-actin binding protein (Fragment).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=98207047; PubMed=9538250;
RA Watanabe A., Kurasawa Y., Watanabe Y., Numata O.;
RT "A new Tetrahymena actin-binding protein is localized in the division
furrow.";
RL J. Biochem. 123:607-613(1998).
CC -!- FUNCTION: BINDS DIRECTLY TO F-ACTIN AND INDUCES ACTIN FILAMENT
BUNDLING. MAY FUNCTION AS A REGULATOR OF ACTIN FILAMENT
CC ORGANIZATION.
CC -!- DEVELOPMENTAL STAGE: CO-LOCALIZED WITH ACTIN IN THE ORAL APPARATUS
IN INTERPHASE CELLS. IN DIVIDING CELLS CO-LOCALIZED WITH ACTIN IN
CC THE DIVISION FURROW.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
7.5, ITS MW IS: 71 kDa.
CC -!- SIMILARITY: TO YEAST FIMBRIN.
KW Actin-binding.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2691 MW; 104FD6FD5E08FD28 CRC64;

Query Match 14.9%; Score 24; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 18 YFKID 22
   : | | | |
Db 2 PFKID 6

RESULT 17
LPT_ECOLI
ID LPT_ECOLI STANDARD; PRT; 21 AA.
AC LP03059;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thr operon leader peptide (Thr operon attenuator).
GN THRL OR B0001.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79201669; PubMed=287010;
RA Gardner J.F.;
RT "Regulation of the threonine operon: tandem threonine and isoleucine
codons in the control region and translational control of
transcription termination.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:1706-1710(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85264808; PubMed=2410621;
RA Lynn S.P., Bauer C.E., Chapman K.A., Gardner J.F.;
RT "Identification and characterization of mutants affecting
transcription termination at the threonine operon attenuator.";
RL J. Mol. Biol. 183:529-541(1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
```

RT region from 92.8 through 100 minutes.";

RL Nucleic Acids Res. 23:2105-2119(1995).

CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS

CC OF THREONINE.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: V00360; CA23658.1; -

DR EMBL: X68872; CA448733.1; -

DR EMBL: J01706; AAA83913.1; -

DR EMBL: M28570; AAA24672.1; -

DR EMBL: U14003; AAA97300.1; -

DR EMBL: AE000111; AAC73112.1; -

DR PIR: A03595; LFECT.

DR Ecogene: EG11277; thrL.

DR Threonine biosynthesis; Leader peptide; Complete proteome.

KW SEQUENCE 21 AA; 2138 MW; 6A9C9167F89EEC4 CRC64;

SQ -----

Query Match 14.9%; Score 24; DB 1; Length 21;

Best Local Similarity 71.4%; Pred. No. 1.8e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLTHTTIT 7

DB 7 TTTTIT 13

RESULT 18

LPTN_ECOLI

ID LPTN_ECOLI STANDARD; PRT; 24 AA.

AC P09408;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tryptophanase leader peptide.

GN TNAL OR TNAC OR B3707 OR Z5202 OR ECS4644.

OS Escherichia coli, and

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562, 83334;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN-K12;

RC MEDLINE=86033634; PubMed=3902796;

RA Stewart V., Yanofsky C.;

RT "Evidence for transcription antitermination control of tryptophanase

RT operon expression in Escherichia coli K-12.";

RL J. Bacteriol. 164:731-740(1985).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN-K12 / MG1655;

RC MEDLINE=93315143; PubMed=7686882;

RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;

RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli

RT genome: organizational symmetry around the origin of replication.";

RL Genomics 16:551-561(1993).

[3]

RN SEQUENCE FROM N.A.

RP STRAIN-O157:H7 / EDL933 / ATCC 700927;

RC MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grobeck E.J., Davis N.W., Lim A., Dimallanta E.T., Potamouis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.;

RL "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

RT Nature 409:529-533(2001).

[4]

RN SEQUENCE FROM N.A.

RP STRAIN-O157:H7 / RIMD 0509952;

RC MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,

RA Kihara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohemorrhagic Escherichia coli

RT O157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: M11990; AAA24678.1; -

DR EMBL: I10328; AAA62058.1; -

DR EMBL: AE000448; AAC76730.1; -

DR EMBL: AE005602; AAG58907.1; -

DR EMBL: AF002566; BAB38067.1; -

DR Ecogene: EG11276; tnal.

KW Leader peptide; Complete proteome.

SQ SEQUENCE 24 AA; 2894 MW; 66E3987EA7C052F9 CRC64;

Query Match 14.9%; Score 24; DB 1; Length 24;

Best Local Similarity 66.7%; Pred. No. 2.1e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 18 YPKIDN 23

DB 12 WFNIDN 17

RESULT 19

PUTA_KLEPN

ID PUTA_KLEPN STANDARD; PRT; 26 AA.

AC P23725;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Bifunctional putA protein [includes: proline dehydrogenase

DE (EC 1.5.99.8) (Proline oxidase); Delta-1-pyrroline-5-carboxylate

DE dehydrogenase (EC 1.5.1.12) (P5C dehydrogenase)] (Fragment).

GN PUTA.

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.

OX NCBI_TaxID=573;

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE=91100369; PubMed=1987164;

RA Chen L.M., Mayo S.;

RT "Regulation of proline utilization in enteric bacteria: cloning and

RT characterization of the Klebsiella put control region.";

RL J. Bacteriol. 173:783-790(1991).

CC -!- FUNCTION: OXIDIZES PROLINE TO GLUTAMATE FOR USE AS A CARBON AND

CC NITROGEN SOURCE AND ALSO FUNCTION AS A TRANSCRIPTIONAL REPRESSOR

CC OF THE PUT OPERON.

CC -!- CATALYTIC ACTIVITY: L-proline + acceptor + H(2)O = (S)-l-

CC pyrroline-5-carboxylate + reduced acceptor.

CC -!- COFACTOR: FAD.

CC -!- PATHWAY: PROLINE UTILIZATION.

CC -!- INDUCTION: BY PROLINE, AUTOREPRESSION AND CATABOLITE REPRESSION,

CC AND IS POTENTIALLY NITROGEN CONTROLLED.

```
CC ----- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63160; AAA25139.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PARTIAL.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; PARTIAL.
KW Multifunctional enzyme; Oxidoreductase; Flavoprotein; FAD; NAD;
KW Transcription regulation; Repressor; DNA-binding; Proline metabolism.
FT NON_TER 26
SQ SEQUENCE 26 AA; 2824 MW; BB332D0DE504CE19 CRC64;

Query Match 14.9%; Score 24; DB 1; Length 26;
Best Local Similarity 26.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 16 TFFFKIDNVKARVQ 30
DB 5 TMGVKLDLTRERIK 19

RESULT 20
AMPT_BACST
ID AMPT_BACST STANDARD; PRT; 30 AA.
AC P00728;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Thermophilic aminopeptidase I alpha chain (EC 3.4.11.-) (Fragment).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 8924;
RX MEDLINE=74087636; PubMed=4521203;
RA Stoll E., Ericsson L.H., Zuber H.;
RT "The function of the two subunits of thermophilic aminopeptidase I.";
RL Proc. Natl. Acad. Sci. U.S.A. 70:3781-3784(1973).
CC -!- FUNCTION: METALLOENZYME OF HIGH TEMPERATURE STABILITY AND OF
CC BROAD SPECIFICITY, RELEASING ALL N-TERMINAL AMINO ACIDS.
CC -!- SUBUNIT: 12 CHAINS OF TWO DIFFERENT BUT HOMOLOGOUS TYPES, ALPHA
CC AND BETA, WHICH CAN COMBINE IN VARIOUS RATIOS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M42.
DR PIR; A00908; AIBSAF.
DR MEROPS; M42.002; -.
KW Hydrolase; Aminopeptidase; Metalloprotease.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3274 MW; D712C9C23E618142 CRC64;

Query Match 14.9%; Score 24; DB 1; Length 30;
Best Local Similarity 42.9%; Pred. No. 2.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LPTITTKLNAENNA 15
DB 3 LDETITLTKALTD 16
```

Search completed: July 8, 2002, 11:53:13
Job time: 199 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:49:19 ; Search time 23.81 Seconds

(Without alignments)
232.501 Million cell updates/sec

Title: US-09-461-061A-4

Perfect score: 161

Sequence: 1 TLTHYTKLNAENNAFFFKIDNVKKARQVV 32

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 14647

Minimum DB seq length: 0

Maximum DB seq length: 32

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	20.5	13	4	Q9UC27
2	32	19.9	27	12	Q9QH83
3	32	19.9	27	12	Q9QH82
4	32	19.9	27	12	Q9QH81
5	32	19.9	27	12	Q9QH80
6	32	19.9	27	12	Q9QH79
7	32	19.9	27	12	Q9QH78
8	32	19.9	27	12	Q9QH77
9	32	19.9	27	12	Q9QH76
10	32	19.9	27	12	Q9QH75
11	32	19.9	27	12	Q9QH74
12	32	19.9	27	12	Q9QH73
13	32	19.9	27	12	Q9QH72
14	32	19.9	27	12	Q9QH70
15	32	19.9	27	12	Q9QH69
16	32	19.9	27	12	Q9QH68

17	32	19.9	27	12	Q9QH66	Q9qh66 hepatitis c
18	32	19.9	32	6	Q9TR69	Q9tr69 sus scrofa
19	32	19.9	32	6	Q9TR67	Q9tr67 sus scrofa
20	31	19.3	23	5	O44207	O44207 onchocerca
21	31	19.3	30	2	O49048	O49048 mycoplasma
22	31	19.3	32	13	Q9W7P3	Q9w7p3 morone saxa
23	30,5	18.9	32	12	Q914F9	Q914f9 sulfolobus
24	30	18.6	23	4	Q96IP0	Q96ip0 homo sapien
25	30	18.6	25	6	Q95L28	Q95l28 canis famli
26	30	18.6	25	16	O26056	O26056 helicobacte
27	30	18.6	26	11	Q9CTD3	Q9ctd3 mus musculu
28	30	18.6	30	4	Q96QY6	Q96qy6 homo sapien
29	30	18.6	31	4	Q9BQU1	Q9bqu1 homo sapien
30	29	18.0	20	13	Q9PSI5	Q9psi5 oncorhynchu
31	29	18.0	23	5	Q9XZW5	Q9xzw5 littorina l
32	29	18.0	23	5	Q9Y003	Q9y003 melarhapse
33	28,5	17.7	29	13	Q90817	Q90817 gallus gall
34	28	17.4	14	5	O26100	O26100 pratylenchu
35	28	17.4	16	5	O26101	O26101 pratylenchu
36	28	17.4	19	5	O26099	O26099 pratylenchu
37	28	17.4	21	2	Q9R585	Q9r585 vibrio. end
38	28	17.4	23	5	Q9XZ27	Q9xzz7 littorina s
39	28	17.4	23	5	Q9XZW1	Q9xzw1 littorina a
40	28	17.4	23	5	Q9XZW4	Q9xzw4 littorina l
41	28	17.4	26	4	Q9UC79	Q9uc79 homo sapien
42	28	17.4	27	12	Q9QRS2	Q9qrs2 hepatitis c
43	28	17.4	27	12	Q9QI47	Q9qi47 hepatitis c
44	28	17.4	27	12	Q9QI44	Q9qi44 hepatitis c
45	28	17.4	27	12	Q9QI41	Q9qi41 hepatitis c

ALIGNMENTS

RESULT 1

Q9UC27 PRELIMINARY; PRT; 13 AA.

AC Q9UC27: Q9UC27: PRELIMINARY; PRT; 13 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 94 KDA EPIDIDYMAL CYTOKERATIN-LIKE PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95226590; Pubmed=7536047;
RA Boue F., Duquenne C., Lassalle B., Lefevre A., Finaz C.;
RT "FBLI, a human protein of epididymal origin that is involved in the
RL sperm-oocyte recognition process.";
RL Biol. Reprod. 52:267-278(1995).
SQ SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;

Query Match 20.5%; Score 33; DB 4; Length 13;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 NNATFFFKIDNVK 25

Db 1 NYSTYNTIDDLK 13

RESULT 2

Q9QH83 PRELIMINARY; PRT; 27 AA.
ID Q9QH83
AC Q9QH83;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)]

DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167045; AAD53678.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLAENNAATF 17
|||: ::: |:
Db 2 THTVGSISRATASF 16

RESULT 3
Q9QH82 PRELIMINARY; PRT; 27 AA.
ID Q9QH82;
AC Q9QH82;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167045; AAD53679.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLAENNAATF 17
|||: ::: |:
Db 2 THTVGSISRATASF 16

RESULT 4
Q9QH81 PRELIMINARY; PRT; 27 AA.
ID Q9QH81

AC Q9QH81;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167047; AAD53680.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLAENNAATF 17
|||: ::: |:
Db 2 THTVGSISRATASF 16

RESULT 5
Q9QH80 PRELIMINARY; PRT; 27 AA.
ID Q9QH80;
AC Q9QH80;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167048; AAD53681.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLAENNAATF 17
|||: ::: |:
Db 2 THTVGSISRATASF 16

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;

SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATF 17
| | | : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 10
Q9QH75 ID Q9QH75 PRELIMINARY; PRT; 27 AA.
AC Q9QH75;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167053; AAD53688.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATF 17
| | | : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 11
Q9QH74 ID Q9QH74 PRELIMINARY; PRT; 27 AA.
AC Q9QH74;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167054; AAD53687.1; -.
DR InterPro; IPR002531; HCV_NS1.

DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2740 MW; D43859586668B361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATF 17
| | | : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 12
Q9QH73 ID Q9QH73 PRELIMINARY; PRT; 27 AA.
AC Q9QH73;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167055; AAD53688.1; -.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATF 17
| | | : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 13
Q9QH72 ID Q9QH72 PRELIMINARY; PRT; 27 AA.
AC Q9QH72;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral

RT genome and the sensitivity of hepatitis C virus to interferon alpha
therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167056; AAD53689.1; -;
DR InterPro: IPR002531; HCV_NSI.
DR Pfam: PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNENATF 17
||| : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 14
Q9QH70
ID Q9QH70 PRELIMINARY; PRT; 27 AA.
AC Q9QH70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
genome and the sensitivity of hepatitis C virus to interferon alpha
therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167058; AAD53691.1; -;
DR InterPro: IPR002531; HCV_NSI.
DR Pfam: PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNENATF 17
||| : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 15
Q9QH69
ID Q9QH69 PRELIMINARY; PRT; 27 AA.
AC Q9QH69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.

OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
genome and the sensitivity of hepatitis C virus to interferon alpha
therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167059; AAD53692.1; -;
DR InterPro: IPR002531; HCV_NSI.
DR Pfam: PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNENATF 17
||| : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 16
Q9QH68
ID Q9QH68 PRELIMINARY; PRT; 27 AA.
AC Q9QH68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
DE (NS1)] (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
genome and the sensitivity of hepatitis C virus to interferon alpha
therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167060; AAD53693.1; -;
DR InterPro: IPR002531; HCV_NSI.
DR Pfam: PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNENATF 17
||| : : : | : |
Db 2 THTVGSISRATASF 16

RESULT 17
Q9QH66
ID Q9QH66 PRELIMINARY; PRT; 27 AA.
AC Q9QH66;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Sandres K., Dubois M., Pasquier C., Izopet J.;
RT "The genetic heterogeneity of the hypervariable region 1 of the viral
RT genome and the sensitivity of hepatitis C virus to interferon alpha
RT therapy.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167062; AAD53695.1; -.
DR InterPro; IPR002531; HCV_N51.
DR Pfam; PF01560; HCV_N51; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;

Query Match 19.9%; Score 32; DB 12; Length 27;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENATF 17
DB 2 THTVGSISRATASF 16

RESULT 18
Q9TR69 PRELIMINARY; PRT; 32 AA.
AC Q9TR69;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE P12 I ALPHA-PROTEASE INHIBITOR (FRAGMENT).
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=95268713; PubMed=7749636;
RA Stratil A., Cizova-Schrofflova D., Gabrisova E., Pavlik M.,
RA Coppieters W., Peelman L., Van de Weghe A., Bouquet Y.;
RT "Pig plasma alpha-protease inhibitors P12, P13 and P14 are members of
RT the antichymotrypsin family.";
RL Comp. Biochem. Physiol. 111B:53-60(1995).
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3442 MW; 467B14B3FB6E72DA CRC64;

Query Match 19.9%; Score 32; DB 6; Length 32;
Best Local Similarity 53.3%; Pred. No. 1.5e+03;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLTHITITKLNAENNA 15
DB 10 TLKQDITKLPHVHTA 24

RESULT 19
Q9TR67 PRELIMINARY; PRT; 32 AA.
AC Q9TR67;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
```

```
DE P14 C2 ALPHA-PROTEASE INHIBITOR (FRAGMENT).
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=95268713; PubMed=7749636;
RA Stratil A., Cizova-Schrofflova D., Gabrisova E., Pavlik M.,
RA Coppieters W., Peelman L., Van de Weghe A., Bouquet Y.;
RT "Pig plasma alpha-protease inhibitors P12, P13 and P14 are members of
RT the antichymotrypsin family.";
RL Comp. Biochem. Physiol. 111B:53-60(1995).
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3464 MW; 4CC602E86D23B2DA CRC64;

Query Match 19.9%; Score 32; DB 6; Length 32;
Best Local Similarity 40.9%; Pred. No. 1.5e+03;
Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLTHITITKLNAENNATFYFKID 22
DB 10 TLKGQIKKLPVNTAVVWXXND 31

RESULT 20
O44207 PRELIMINARY; PRT; 23 AA.
AC O44207;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTIGEN (FRAGMENT).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FOREST;
RA Titanji V.P.K., Sakwe A.M., Ghogomu S.M., Souopgui J., Djokam R.T.,
RA Perlier F., Rask L.;
RT "A CDNA coding for a novel antigen from Onchocerca volvulus.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15982; CAA75807.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 23 AA; 2777 MW; CA40C0430F5F1F54 CRC64;

Query Match 19.3%; Score 31; DB 5; Length 23;
Best Local Similarity 35.3%; Pred. No. 1.5e+03;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 4 HTITKLNAENNATFYFK 20
DB 4 HINDYLDTNHNADYVLK 20

Search completed: July 8, 2002, 11:52:56
Job time: 217 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:47:19 ; Search time 29.33 Seconds
(without alignments)
121.185 Million cell updates/sec

Title: US-09-461-061A-4

Perfect score: 161

Sequence: 1 TLHTTTLKNAENNAIFPKIDNVKARQVV 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 285274

Minimum DB seq length: 0

Maximum DB seq length: 32

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	32	21 AAY95408	Anti-angiogenic D3
2	95	59.0	26	18 AAW54336	Bradykinin analogo
3	84	52.2	16	21 AAY95410	Anti-angiogenic D3
4	83	51.6	16	21 AAY95409	Anti-angiogenic D3
5	74	46.0	16	21 AAB08553	Peptide identified
6	60	37.3	12	21 AAY95406	Anti-angiogenic pe
7	56	34.8	12	21 AAY95407	Anti-angiogenic pe
8	49	30.4	9	21 AAB37455	Human kininogen D3
9	45	28.0	10	21 AAY95405	Human kininogen D3
10	40	24.8	32	20 AAW94743	Anti-angiogenic D3
11	39	24.2	32	13 AAR27043	Anti-Staph (HAY) 9 Human light chain

12	39	24.2	32	16	AAR85155	Human ONS-M21 anti
13	39	24.2	32	16	AAR77206	Mouse anti-human I
14	39	24.2	32	17	AAR96288	Light chain framew
15	39	24.2	32	17	AAR97321	Humanised monoclon
16	37	23.0	32	17	AAR87043	Human group I ligh
17	37	23.0	32	20	AAY52745	Humanised ATR-5 L
18	37	23.0	32	20	AAY52745	Humanised ATR-5 L
19	37	23.0	32	20	AAY52747	Humanised ATR-5 L
20	37	23.0	32	22	AAB98286	Anti-A33 antigen i
21	37	23.0	32	22	AAB98287	Anti-A33 antigen i
22	37	23.0	32	22	AAB98288	Anti-A33 antigen i
23	37	23.0	32	22	AAB97666	A33 antigen bindin
24	37	23.0	32	22	AAB97667	A33 antigen bindin
25	37	23.0	32	22	AAB97668	A33 antigen bindin
26	36.5	22.7	24	22	AAO04947	Human polypeptide
27	36	22.4	18	15	AAW47004	Ig kappa chain pos
28	35	21.7	7	18	AAW54340	Bradykinin analogo
29	35	21.7	7	19	AAW77428	Peptide LNA7, a no
30	35	21.7	22	18	AAW17883	Photorehabdus lumin
31	35	21.7	22	19	AAW56565	Toxin fragment of
32	35	21.7	27	12	AAAR10432	CD4 fragment pepti
33	35	21.7	27	14	AAAR10432	HIV superinfection
34	35	21.7	32	22	AAB98290	Anti-A33 antigen i
35	35	21.7	32	22	AAB97670	A33 antigen bindin
36	34	21.1	21	21	AAW94747	Non-malignant exo
37	34	21.1	28	21	AAW89463	Core polypeptide f
38	34	21.1	28	22	ABG18695	Novel human diago
39	34	21.1	28	22	ABB00871	Viral DPI78/107-11
40	34	21.1	28	22	ABB02346	Viral core polypep
41	34	21.1	28	22	AAU13417	DP178-like/DPI07-1
42	34	21.1	28	22	AAB77864	Core polypeptide T
43	34	21.1	30	19	AAW73005	Cobra venom mocrar
44	34	21.1	31	20	AAY30773	Vasoactive inteçtl
45	34	21.1	32	17	AAR97330	Humanised monoclon

ALIGNMENTS

RESULT 1

AAW95408

ID AAY95408 standard; Peptide; 32 AA.

AC AAY95408;

XX 25-SEP-2000 (first entry)

DE Anti-angiogenic D3 peptide.

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

OS Homo sapiens.

XX WO200035407-A2.

XX 22-JUN-2000.

XX 02-DEC-1999; 99WO-US28465.

XX 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.

XX (MCCR/) MCCRAE R K.

XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell

XX proliferation, inducing endothelial cell apoptosis and treating cancer,

Ward

PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog -

PS Claim 4; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human
XX high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
CC inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of D3 peptides of the
CC invention (see AAY95405-26) that are analogues of certain sites in
CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
CC The peptides inhibit endothelial cell proliferation and may also
CC induce endothelial cell apoptosis. Compositions including the
CC peptides are used in claimed methods for inhibiting angiogenesis,
CC inhibiting endothelial cell proliferation, and inducing endothelial
CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
CC characterized by undesired vascularization of the retina are treated.

XX Sequence 32 AA;

Query Match 100.0%; Score 161; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e-15; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;

QY 1 TLTHITITKINAENNATFYFKIDNVKKARQVV 32
Db 1 tlthititkinaennatfykldnvkkrvqv 32

RESULT 2

AAW54336
ID AAW54336 standard; peptide; 26 AA.

XX AC AAW54336;

XX DT 30-JUL-1998 (first entry)

XX DE Bradykinin analogous peptide 19.

XX KW Inhibition; thrombin-induced platelet; prevention; platelet aggregation;
XX ADP-induced activation.

XX OS Synthetic.

XX PN W09641640-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09940.

XX PR 09-JUN-1995; 95US-0000096.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Hasan AAK, Schmaier AH;

XX DR WPT; 1997-065304/06.

XX PT Inhibition of platelet activation and aggregation - by admin. of new
XX or known bradykinin analogues

XX PS Disclosure; Page 44; 73pp; English.

XX CC Administration of a peptide or multimer related to bradykinin or other
XX disclosed peptides and multimers can be used for the inhibition of
XX thrombin-induced platelets or other cells. They can also be used for
XX preventing platelet aggregation, or inhibiting ADP-induced activation.
XX This is useful to prevent arterial occlusions arising from coronary
XX thrombosis and stroke.

XX Sequence 26 AA;

Query Match 59.0%; Score 95; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 NATFYFKIDNVKKARQVV 32
Db 1 natfyfkldnvkkrvqv 19

RESULT 3

AAAY95410
ID AAY95410 standard; Peptide; 16 AA.

XX AC AAY95410;

XX DT 25-SEP-2000 (first entry)

XX DE Anti-angiogenic D3 peptide.

XX KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;
XX rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
XX therapy; human; D3 peptide.

XX OS Homo sapiens.

XX PN W0200035407-A2.

XX PD 22-JUN-2000.

XX PF 02-DEC-1999; 99WO-US28465.

XX PR 16-DEC-1998; 98US-0112427.

XX PA (UTEM) UNIV TEMPLE.

XX PI (MCCR/) MCCRAE R K.

XX PI McCrae RK;

XX DR WPT; 2000-442247/38.

XX PT Composition for inhibiting angiogenesis and endothelial cell
XX proliferation, inducing endothelial cell apoptosis and treating cancer,
XX rheumatoid arthritis, and ocular disorders comprises a kininogen domain
XX 3 analog

XX PS Claim 7; Page 26; 44pp; English.

XX CC The present sequence is that of a D3 peptide derived from human
XX high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
XX inhibits endothelial cell proliferation and thus possesses
XX anti-angiogenic activity. It is an example of D3 peptides of the
XX invention (see AAY95405-26) that are analogues of certain sites in
XX the HK domain 3, in this case amino acid residues Asn275-Lys282.
XX The peptides inhibit endothelial cell proliferation and may also
XX induce endothelial cell apoptosis. Compositions including the
XX peptides are used in claimed methods for inhibiting angiogenesis,
XX inhibiting endothelial cell proliferation, and inducing endothelial
XX cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
XX characterized by undesired vascularization of the retina are treated.
XX The IC50 value for the present peptide was less than 0.8 uM for
XX inhibition of fibroblast growth factor-induced HUVEC cell
XX proliferation.

XX SQ Sequence 16 AA;

Query Match 52.2%; Score 84; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NNATFYFKIDNVKKAR 28

Db 1 nnatyfkidnvkxar 16

RESULT 4

AA95409
ID AAY95409 standard; Peptide: 16 AA.

AC AAY95409;

DT 25-SEP-2000 (first entry)

DE Anti-angiogenic D3 peptide.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

OS Homo sapiens.

XX WO200035407-A2.

PN 22-JUN-2000.

PD 02-DEC-1999; 99WO-US28465.

PF 16-DEC-1998; 98US-011247.

PR (UTEM) UNIV TEMPLE.

PA (MCCR) MCCRAE R. K.

XX McCrae RK;

PI WPI; 2000-442247/38.

DR Composition for inhibiting angiogenesis and endothelial cell

PT proliferation, inducing endothelial cell apoptosis and treating cancer,

PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain

PT 3 analog

XX Claim 6; Page 26; 44pp; English.

CC The present sequence is that of a D3 peptide derived from human

CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide

CC inhibits endothelial cell proliferation and thus possesses

CC anti-angiogenic activity. It is an example of D3 peptides of the

CC invention (see AAY95405-26) that are analogues of certain sites in

CC the HK domain 3, in this case amino acid residues Asn275-Lys282.

CC The peptides inhibit endothelial cell proliferation and may also

CC induce endothelial cell apoptosis. Compositions including the

CC peptides are used in claimed methods for inhibiting angiogenesis,

CC inhibiting endothelial cell proliferation, and inducing endothelial

CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders

CC characterized by undesired vascularization of the retina are treated.

CC The IC50 value for the present peptide was less than 0.8 uM for

CC inhibition of fibroblast growth factor-induced HUVEC cell

XX proliferation.

XX Sequence 16 AA;

Query Match

Best Local Similarity 51.6%; Score 83; DB 21; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TITKLNANNATFYFK 20

Db 1 titklnaennatfyk 16

RESULT 5

AAB08553

ID AAB08553 standard; Peptide: 16 AA.

AC AAB08553;

DT 20-DEC-2000 (first entry)

DE Peptide identified from an origin of prepro-bradykinine.

KW Precursor peptide; polypeptide hormone; peptide identification.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "hydrogen attached"

FT Modified-site 16

FT /note= "amidated residue"

XX WO200050636-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-FR00460.

XX 25-FEB-1999; 99US-0257525.

XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Camara Ferrer YJA, Thureau C, Martinez J, Berge G, Goze C;

XX WPI; 2000-572101/53.

XX Identifying peptide with selected function, useful particularly for
PT C-amidated hormones, by screening database for combination of nucleic
PT acid and amino acid sequences

XX Claim 16; Page 20; 40pp; French.

XX The specification describes a method for identifying a peptide having
CC a particular function. The method comprises preparing a database of
CC polynucleotides and polypeptides of unknown functions, screening the
CC database for a combination of nucleotides or amino acids indicative of
CC the peptide with a particular function, and identifying polynucleotides
CC and proteins which contain the peptide. The method is used to identify
CC precursor peptides with an amidated C-terminus, especially polypeptide
CC hormones, for studying physiologically active substances. The present
CC sequence represents a peptide which was identified using the method of
CC the invention.

XX Sequence 16 AA;

Query Match 46.0%; Score 74; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 YFKIDNVKKARVQV 32

Db 1 yfkidnvkkrvqv 15

RESULT 6

AA95406

ID AAY95406 standard; Peptide: 12 AA.

XX AAY95406;

XX 25-SEP-2000 (first entry)

XX Anti-angiogenic peptide N-terminal fragment.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
KW therapy; human; D3 peptide.
XX
OS Homo sapiens.
XX
PN WO200035407-A2.
XX
XX
PD 22-JUN-2000.
XX
XX
PF 02-DEC-1999; 99WO-US28465.
XX
XX
PR 16-DEC-1998; 98US-0112427.
XX
XX
PA (UTEM) UNIV TEMPLE.
PA (MCCR/) MCCRAE R K.
XX
XX
PI McCrae RK;
XX
XX
DR WPI; 2000-442247/38.
XX
XX
PT Composition for inhibiting angiogenesis and endothelial cell
PT proliferation, inducing endothelial cell apoptosis and treating cancer,
PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog -
XX
XX
PS Claim 3; Page 25; 44pp; English.
XX
XX
CC The present sequence is that of an N-terminal fragment of a novel
CC anti-angiogenic D3 peptide (see AAY95408) derived from human high
CC mol.wt. kininogen (HK) domain 3 (see AAY95426). The full-length D3
CC peptide inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of peptides of the
CC invention (see AAY95405-26) that are analogues of certain sites in
CC the HK domain 3. The peptides inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.
XX
XX
SQ Sequence 12 AA;

Query Match 37.3%; Score 60; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLTHPTITKLNAE 12
Db 1 tlthtktklnae 12
|||||
1 tlthtktklnae 12

RESULT 7
AAY95407
ID AAY95407 standard; Peptide; 12 AA.
XX
XX
AC AAY95407;
XX
XX
DT 25-SEP-2000 (first entry)
XX
XX
DE Anti-angiogenic peptide C-terminal fragment.
XX
KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
KW therapy; human; D3 peptide.
XX
OS Homo sapiens.
XX
PN WO200035407-A2.
XX

PD 22-JUN-2000.
XX
XX
PF 02-DEC-1999; 99WO-US28465.
XX
XX
PR 16-DEC-1998; 98US-0112427.
XX
XX
PA (UTEM) UNIV TEMPLE.
PA (MCCR/) MCCRAE R K.
XX
XX
PI McCrae RK;
XX
XX
DR WPI; 2000-442247/38.
XX
XX
PT Composition for inhibiting angiogenesis and endothelial cell
PT proliferation, inducing endothelial cell apoptosis and treating cancer,
PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog -
XX
XX
PS Claim 3; Page 25; 44pp; English.
XX
XX
CC The present sequence is that of a C-terminal fragment of a novel
CC anti-angiogenic D3 peptide (see AAY95408) derived from human high
CC mol.wt. kininogen (HK) domain 3 (see AAY95426). The full-length D3
CC peptide inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of peptides of the
CC invention (see AAY95405-26) that are analogues of certain sites in
CC the HK domain 3. The peptides inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.
XX
XX
SQ Sequence 12 AA;

Query Match 34.8%; Score 56; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 IDNVKKARQVV 32
Db 1 idnvkkrvqv 12
|||||
1 idnvkkrvqv 12

RESULT 8
AAB37455
ID AAB37455 standard; peptide; 9 AA.
XX
XX
AC AAB37455;
XX
XX
DT 21-FEB-2001 (first entry)
XX
XX
DE Human kininogen D3 peptide fragment.
XX
KW Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
XX
XX
OS Homo sapiens.
XX
PN WO200064945-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 20-APR-2000; 2000WO-GB01571.
XX
XX
PR 22-APR-1999; 99GB-0009133.
XX
XX
PA (BABR-) BABRAHAM INST.
XX
XX
PI Abrahamson M, Barrett AJ;
XX
XX
DR WPI; 2000-687316/67.

XX Inhibition of mammalian legumain or legumain-related endopeptidase by
PT cystatin involves interaction with second papain-non-reactive site of
PT cystatin
XX
PS Disclosure; Fig 4; 45pp; English.
XX
CC The present invention relates to inhibition of the enzymatic activity of
CC legumain or a legumain-related endopeptidase by cystatin. The inhibition
CC involves an interaction between legumain and a papain-non-reactive site
CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
CC performs a protein-processing function. The present invention is a peptide
CC fragment of human kininogen D3, which was used in the present invention.
CC Kininogen is a type 3 cystatin. The present sequence is thought to be
CC involved in a legumain-inhibitory site.
XX
SQ Sequence 9 AA;

Query Match 30.4%; Score 49; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NNATYFKI 21
DB 1 nnatfyfki 9

RESULT 9
AAAY95405
ID AAY95405 standard; Peptide; 10 AA.
XX
AC AAY95405;
XX
DT 25-SEP-2000 (first entry)
XX
DE Anti-angiogenic D3 peptide.
XX
KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
KW therapy; human; D3 peptide.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Xaa represents 0 amino acids, or the
FT sequence of AAY95406 or its N-terminal
FT truncation fragment containing at least
FT 1 amino acid"
FT
FT Peptide 2..9
FT /note= "corresponds to residues Asn(275)-Lys(282)
FT of HK domain 3"
FT
FT Misc-difference 10
FT /note= "Xaa represents 0 amino acids, or the
FT sequence of AAY95407 or its C-terminal
FT truncation fragment containing at least
FT 1 amino acid"
XX
XX WO200035407-A2.
XX
XX 22-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US28465.
XX
XX 16-DEC-1998; 98US-0112427.
XX
XX (UTEM) UNIV TEMPLE.
PA (MCCR/) MCCRAE R K.
XX
PI McCrae RK;
XX

DR WPI; 2000-442247/38.
XX Composition for inhibiting angiogenesis and endothelial cell
PT proliferation, inducing endothelial cell apoptosis and treating cancer,
PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog
XX
PS Claim 1; Page 25; 44pp; English.
XX
CC The present sequence is that of a D3 peptide derived from high
CC mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide, which
CC may optionally include N-terminal and/or C-terminal protecting
CC groups, inhibits endothelial cell proliferation and thus possesses
CC anti-angiogenic activity. It is an example of peptides of the
CC invention (see AAY95405-26) which are analogues of certain sites in
CC the HK domain 3, in this case amino acids Asn275-Lys282. The
CC peptides inhibit endothelial cell proliferation and may also induce
CC endothelial cell apoptosis. Compositions including such peptides
CC are used in claimed methods for inhibiting angiogenesis, inhibiting
CC endothelial cell proliferation, and inducing endothelial cell
CC apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
CC characterized by undesired vascularization of the retina are treated.
XX
SQ Sequence 10 AA;

Query Match 28.0%; Score 45; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NNATYFKK 20
DB 2 nnatfyfk 9

RESULT 10
AAW94743
ID AAW94743 standard; Protein; 32 AA.
XX
AC AAW94743;
XX
DT 22-APR-1999 (first entry)
XX
DE Anti-Staph (HAY) 96-110 light chain variable region.
XX
KW Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW MAb 96-110.
XX
OS Mus sp.
XX
XX WO9857994-A2.
XX
XX 23-DEC-1998.
XX
XX 16-JUN-1998; 98WO-US12402.
XX
XX 16-JUN-1997; 97US-0049871.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
XX Fischer GW, Schuman RF, Stinson JL, Wong H;
XX WPI; 1999-095329/08.
DR N-PSDB; AAX05587.
XX
XX New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
XX Claim 21; Fig 12; 150pp; English.
XX
XX The invention relates to a monoclonal antibody (MAb) to lipoteichoic
CC

CC acid of gram positive bacteria, where the MAB is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC antibodies or peptides (encoded by a DNA of the variable region of
CC anti-lipoteichoic acid antibody or characterised by amino acids
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAM94740-44 represent light chain variable regions of the
CC anti-lipoteichoic antibody 96-100.

XX Sequence 32 AA;

Query Match 24.2%; Score 40; DB 20; Length 32;
Best Local Similarity 50.0%; Pred. NO. 1.2e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TITKLNAENNATFY 18
||::||:||:|
Db 18 tlrveaeadaaty 31

RESULT 11
AAR27043
ID AAR27043 standard; peptide; 32 AA.

XX AC AAR27043;

XX DT 01-MAR-1993 (first entry)

XX DE Human light chain framework 3 used in humanised MAB.

XX KW Monoclonal antibody; complementarity determining region; CDR;
XX antigens; tumour; melanoma; carcinoma; glioma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX Misc-difference 15
XX /label= Tyr, Phe, Trp, His

XX PN WO9215683-A.

XX PD 17-SEP-1992.

XX PF 04-MAR-1992; 92WO-EP00480.

XX PR 06-MAR-1991; 91EP-0103389.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Bendig MM, Kettleborough CA, Saldanha J;

XX DR WPI; 1992-331729/40.

XX PT Human monoclonal antibodies binding to human receptors - for
XX treatment and diagnosis of tumours, e.g. melanoma and carcinoma

XX PS Claim 5; Page 63; 89pp; English.

XX CC The human framework sequence PR3 was used in the prodn. of
XX humanised monoclonal antibodies comprising antigen binding sites
XX (CDRs) of non human origin based on consensus sequence of CDRs.
XX The sequence is a light chain framework region. The humanised
XX antibodies or their chimeric variants may be used as therapeutic
XX or diagnostic agents in order to combat e.g. glioma, melanoma or
XX carcinoma. See also AAR27299-300 and AAR27037-51.

SQ Sequence 32 AA;

Query Match 24.2%; Score 39; DB 13; Length 32;
Best Local Similarity 50.0%; Pred. NO. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNATFY 18
|::|::|::|
Db 16 tftisslqpdiaty 31

RESULT 12
AAR85155
ID AAR85155 standard; Protein; 32 AA.

XX AC AAR85155;

XX DT 18-JAN-1996 (first entry)

XX DE Human ONS-M21 antibody light variable region FR 3;

XX KW Human; ONS-M21 antibody; light variable region; chimeric protein;
XX framework region; FR 3; medulloblastoma; brain tumour; treatment;
XX diagnosis.

XX OS Homo sapiens.

XX PN WO9514041-A1.

XX PD 26-MAY-1995.

XX PF 19-OCT-1994; 94WO-JP01763.

XX PR 19-NOV-1993; 93JP-0291078.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Ohtomo T, Sato K, Tsuchiya M;

XX DR WPI; 1995-200347/26.

XX PT Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity

XX PS Claim 9; Page 101; 120pp; Japanese.

XX CC AAR85153-R85156 are human antibody ONS-M21 light variable region
XX framework regions (FRs). They were used in the construction of
XX a human/murine chimeric antibody, reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.

XX SQ Sequence 32 AA;

Query Match 24.2%; Score 39; DB 16; Length 32;
Best Local Similarity 50.0%; Pred. NO. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNATFY 18
|::|::|::|
Db 16 tftisslqpdiaty 31

RESULT 13
AAR77206
ID AAR77206 standard; Peptide; 32 AA.

XX AC AAR77206;

XX DT 23-AUG-1995 (first entry)

XX Mouse anti-human IL-6 Ab L chain V region framework region 3.
DE Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
KW interleukin; antibody; hybridoma; CDR; framework; constant region;
KW heavy chain; disorder; antigenicity.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 15
FT /label= Phe or Tyr
FT /*note= "In HEF-RVL-SK2a, this position is Phe;
FT in HEF-RVL-SK2b, this position is Tyr"
XX
XX WO9428159-A.
XX
XX 08-DEC-1994.
XX
XX 30-MAY-1994; 94WO-JP00859.
XX
XX 31-MAY-1993; 93JP-0129787.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
XX (CHUS) CHUGAI PHARM CO LTD.
XX
PI Hirata Y, Sato K, Tsuchiya M;
XX
XX WPI; 1995-022828/03.
XX
XX Antibody against IL-6 - useful for the therapy and treatment of
XX IL-6 related disorders.
XX
XX Claim 6; Page 64; 82pp; Japanese.
XX
XX The sequence of the mouse anti-human interleukin-6 (IL-6) antibody light
XX chain variable region framework region (FR) 3. The sequences of FR1-4
XX (AA077204-7) were used in conjunction with the complementarity
XX determining regions 1-3 (AA077201-3) to construct a chimeric antibody
XX against human interleukin-6 (IL-6). The vectors AAQ75914-7 express
XX constructs encoding fragments of a chimeric antibody to the human IL-6
XX comprising (a) a light chain with (i) a variable region containing 3 CDR
XX (AA077201-3) inserted into several framework regions (FR) (AA077204-7)
XX and (ii) a human light chain constant region and (b) a heavy chain with
XX (i) a variable region containing 3 CDR (AA077212-4) inserted into FR
XX (AA077215-8) and (ii) a human light chain constant region. The FR of the
XX light chain may be mouse derived (AAQ75888) or from the human antibody
XX REI. The heavy chain FR may also be mouse derived (AAQ75889) or from the
XX human antibody DAW. The antibodies can be used in the treatment of IL-6
XX related disorders. The antibodies are useful as they have low
XX antigenicity due to the use of human derived sequences and low
XX antigenicity mouse derived sequences.
SQ Sequence 32 AA;

Query Match 24.2%; Score 39; DB 16; Length 32;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNNAENNATFY 18
Db 16 tfttsslpqdiatyy 31

RESULT 14
AA096288
ID AAR96288 standard; peptide; 32 AA.
XX
AC AAR96288;
XX
DT 07-JAN-1997 (first entry)
XX

Query Match 24.2%; Score 39; DB 17; Length 32;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNNAENNATFY 18
Db 16 tfttsslpqdiatyy 31

RESULT 15
AAR97321
ID AAR97321 standard; peptide; 32 AA.
XX
AC AAR97321;
XX
DT 15-OCT-1996 (first entry)
XX
XX Humanised monoclonal antibody light chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen;
KW CEA; diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.

DE Light chain framework region 3 for human EGF-R antibody.
XX
KW Antibody; Ab; human; EGF-R; epidermal growth factor receptor; monoclonal;
KW humanised antibody; framework region; antigen binding site; light chain;
KW CDR; heavy chain; gamma-1 chain; kappa chain; immunoglobulin; epithelium;
KW malignant tumour; breast; bladder; ovary; colon; lung; brain; oesophagus;
KW therapy.
XX
OS Synthetic.
XX
PN EP712863-A1.
XX
PD 22-MAY-1996.
XX
XX 15-NOV-1995; 95EP-0203126.
XX
XX 18-NOV-1994; 94CU-0000128.
XX
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
XX Frias EM, Mateo Del Acosta Del Rio CM, Rodriguez RP;
PI WPI; 1996-252836/26.
XX
XX Humanised and chimeric antibodies for EGF receptor - used in
XX diagnosis and therapy of tumours
XX
XX Claim 6; Page 12; 24pp; English.
XX
XX AAR96286-R96293 represent framework regions (FR) for a humanised
XX monoclonal antibody (Ab) specific for the human epidermal growth factor
XX (EGF) receptor. This Ab binds to human EGF-R, and inhibits binding of
XX EGF to the EGF-R. The humanised Ab comprises antigen binding sites
XX (CDR's) of non-human origin, and FRs of the variable and constant regions
XX of light and heavy chains of human origin. The constant heavy chain
XX region used comprises the amino acid sequence of a gamma-1 chain. The
XX constant light chain region used comprises the kappa chain of a human
XX immunoglobulin. High levels of EGF-R have been detected in malignant
XX tumours originating in the epithelium. These include breast tumours,
XX bladder tumours, ovarian tumours, colonic tumours, lung tumours, brain
XX tumours and tumours of the oesophagus. The presence of EGF-R in tumour
XX cells is an indicator of a poor prognosis (particularly in human breast
XX cancer). The Ab can therefore be used for diagnostic localisation and
XX assessment of tumour growth. The Ab can also be used in the design of a
XX drug targeted to the tumour.
SQ Sequence 32 AA;

Query Match 24.2%; Score 39; DB 17; Length 32;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNNAENNATFY 18
Db 16 tfttsslpqdiatyy 31

RESULT 15
AAR97321
ID AAR97321 standard; peptide; 32 AA.
XX
AC AAR97321;
XX
DT 15-OCT-1996 (first entry)
XX
XX Humanised monoclonal antibody light chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen;
KW CEA; diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.

```
XX FH Key Location/Qualifiers
XX FT Misc-difference 4
XX FT /note= "Serine or Aspartic acid."
XX FT Misc-difference 10
XX FT /note= "Glycine or Valine."
XX XX
XX PN WO9611013-Al.
XX PD 18-APR-1996.
XX XX
XX PF 28-SEP-1995; 95WO-US11964.
XX XX
XX PR 05-OCT-1994; 94US-0318157.
XX XX
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Armour KL, Hansen HJ;
XX XX
XX DR WPI; 1996-209653/21.
XX XX
XX PT New humanised anti-CEA monoclonal antibody - having engrafted murine
XX PT CDRs, used for diagnosis, imaging and therapy of CEA-producing
XX PT cancers
XX XX
XX PS Claim 7; Page 39; 62pp; English.
XX XX
XX CC New humanised monoclonal antibodies (MABs) comprising the
XX CC complementary determining regions (CDRs) of a parental murine class
XX CC III anti-carcinoembryonic (CEA) MAB engrafted to the framework
XX CC regions (FRs) of a heterologous antibody which can be derived from
XX CC any species including human, retain the anti-CEA binding specificity
XX CC of the parental murine MAB but are less immunogenic in a human
XX CC subject than the parental MAB. The humanised antibodies can be used
XX CC in diagnosis, imaging and therapy of CEA-producing cancers and
XX CC patients receiving the humanised antibodies and conjugates show
XX CC improved therapeutic results, decreased immune responses and
XX CC decreased immune-mediated adverse effects compared to the parent
XX CC antibody. This sequence corresponds to the third framework region
XX CC of the light chain of the humanised MAB. See AAR97313-97333.
XX XX
XX SQ Sequence 32 AA;

Query Match 24.2%; Score 39; DB 17; Length 32;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATFY 18
Db 16 tftisslqpediatyy 31

RESULT 16
AAR87043
ID AAR87043 standard; Peptide; 32 AA.
XX AC AAR87043;
XX DT 25-JUN-1996 (first entry)
XX XX
XX DE Human group I light chain framework 3.
XX XX
XX KW Humanised antibody; interleukin-5; IL-5; recombinant antibody;
XX KW antibody engineering; monoclonal antibody; MAB; 39D10; CDR;
XX KW complementarity determining region; light chain; framework;
XX KW eosinophilia; allergy; asthma.
XX OS Homo sapiens.
XX XX
XX PN WO9535375-Al.
XX XX
XX PD 28-DEC-1995.
```

```
XX XX 16-JUN-1995; 95WO-GB01411.
XX PF
XX XX 17-JUN-1994; 94GB-0012230.
XX PR
XX XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX PA
XX XX Athwal DS, Bodmer MW, Entage JS;
XX PI
XX XX WPI; 1996-058412/06.
XX DR
XX XX
XX XX Anti-human IL-5 recombinant antibody - useful for preventing or
XX PT reducing eosinophilia and for treating certain allergic diseases,
XX PT esp. asthma
XX XX
XX PS Example 3; Fig 3; 69pp; English.
XX XX
XX CC Framework regions (AAR87041-44) of human group I (gpI) germ line
XX CC antibody light chain showed homology to corresponding regions
XX CC (AAR87045-48, respectively) of the rat anti-human interleukin-5
XX CC monoclonal antibody 39D10 light chain (see AAR87040). This homology
XX CC was utilised in the prodn. of a humanised 39D10 VL (AAR87057) in
XX CC which rat 39D10 VL complementarity determining regions were grafted
XX CC into the human gpI framework.
XX XX
XX SQ Sequence 32 AA;

Query Match 23.0%; Score 37; DB 17; Length 32;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 THTITKLNAENNATFY 18
Db 16 tltisslqpediatyy 31

RESULT 17
AAY52745
ID AAY52745 standard; Peptide; 32 AA.
XX AC AAY52745;
XX XX
XX DT 26-JAN-2000 (first entry)
XX XX
XX DE Humanised ATR-5 L chain V region FR3 for "a".
XX XX
XX KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
XX KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
XX KW disseminated intravascular coagulation; immunogenicity; chimeric.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9951743-Al.
XX XX
XX PD 14-OCT-1999.
XX XX
XX PF 02-APR-1999; 99WO-JP01768.
XX XX
XX PR 03-APR-1998; 98JP-0091850.
XX XX
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX XX
XX PL Sato K, Adachi H, Yabuta N;
XX XX
XX XX WPI; 1999-620204/53.
XX DR
XX XX Humanised antibody recognizing human tissue factor, used for treatment
XX PT of disseminated intravascular coagulation -
XX PT Claim 17; Page 270; 291pp; Japanese.
XX PS
XX XX
```

CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hTF) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 CC chains containing the variable region of the L chain of a mouse
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hTF binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 CC AA52767 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 32 AA;

Query Match 23.0%; Score 37; DB 20; Length 32;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNATFY 18
 | | | | | | | | | |
 Db 16 tlttisslqpdfatyy 31

RESULT 18

AA52746
 ID AAY52746 standard; Peptide; 32 AA.

XX AAY52746;

XX 26-JAN-2000 (first entry)

XX Humanised ATR-5 L chain V region FR3 for "b", "b1" and "b2".

XX Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 disseminated intravascular coagulation; immunogenicity; chimeric.

XX Synthetic.

XX Homo sapiens.

XX WO9951743-A1.

XX 14-OCT-1999.

XX 02-APR-1999; 99WO-JP01768.

XX 03-APR-1998; 98JP-0091850.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Adachi H, Yabuta N;

XX WPI; 1999-620204/53.

XX Humanised antibody recognizing human tissue factor, used for treatment
 of disseminated intravascular coagulation -

XX Claim 17; Page 270; 291pp; Japanese.

XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hTF) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 CC chains containing the variable region of the L chain of a mouse

CC monoclonal Ab recognising human tissue factor (hTF) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hTF binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 CC AA52767 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 32 AA;

Query Match 23.0%; Score 37; DB 20; Length 32;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 THTITKLNAENNATFY 18
 | | | | | | | | | |
 Db 16 tlttisslqpdfatyy 31

RESULT 19

AA52747
 ID AAY52747 standard; Peptide; 32 AA.

XX AAY52747;

XX 26-JAN-2000 (first entry)

XX Humanised ATR-5 L chain V region FR3 for "c".

XX Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 disseminated intravascular coagulation; immunogenicity; chimeric.

XX Synthetic.

XX Homo sapiens.

XX WO9951743-A1.

XX 14-OCT-1999.

XX 02-APR-1999; 99WO-JP01768.

XX 03-APR-1998; 98JP-0091850.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Adachi H, Yabuta N;

XX WPI; 1999-620204/53.

XX Humanised antibody recognizing human tissue factor, used for treatment
 of disseminated intravascular coagulation -

XX Claim 17; Page 271; 291pp; Japanese.

XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hTF) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 CC chains containing the variable region of the L chain of a mouse
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hTF binding activity of the mouse monoclonal antibody but

CC greatly reduced immunogenicity. AAZ33001 to AAZ33091 and Y527007 to
CC AAY52767 represent sequences used in the exemplification of the present
CC invention.

Query Match 23.0%; Score 37; DB 20; Length 32;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels

Qy 3 THTITKLAENNATFY 18
| | | : | | : | | : |
Db 16 tltisslqpdiaty 31

RESULT 20

RESUL 20
AAB98286
ID AAB98286 standard; Peptide; 32 AA.

AA
AC AAB98286;

20-AUG-2001 (first entry)

DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.

AA Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW Immunoglobulin; complementarity determining region; CDR; cancer;
KW cytostatic; anticancer; colon cancer; stomach cancer.

OS Homo sapiens.

AA
PN
WO200130393-A2.

03-MAY-2001.

20-OCT-2000: 2000WO-US29289.

XX 22-OCT-1999: 99US-0425638.

PK 22-OCT-1999; 990US-0425038;
PR 04-APR-2000; 2000US-0543004.

PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (Scripps Res Inst.

PI Barbas CF, Rader C, Ritter G, Welt S, old LJ;

DR WPI; 2001-328613/34.

AA
PT
PT
PT
PT

Treating cancers, particularly of stomach and colon, that express A33 antigen by administering conjugate of anticancer agent with specific immunoglobulin product -

Claim 16; Page 40; 85pp; English.

The present invention describes a method for treating cancers that express the A33 antigen. The method comprises administering an anticancer agent (I) conjugated to an immunoglobulin product (II) that binds specifically to A33 and contains one or more of 13 specified complementarity determining regions (CDRs), given in AAB98262 to CC AAB98274. (I) has cytostatic activity. The method can be used for CC treating colon and stomach cancers. (II), or the nucleic acid encoding CC it, can be used directly, in unconjugated form, for immunotherapy of CC cancer, and, when labeled, for detection or diagnosis of diseases CC associated with A33 expression. AAB22218 to AAB22254 and AAB98230 to CC AAB98321 represent sequences used in the exemplification of the CC present invention.

Query Match	23.0%	Score 37;	DB 22;	Length 32;
Best Local Similarity	50.0%	Pred. No.	3.1e+02.	

	Matches	8; Conservative
QY	3	THTITKLNNAENNATFY 18
		: :
Db	16	tltlssllqpedvatyy 31

Search completed: July 8, 2002, 11:49:53
Job time: 154 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:37:53 ; Search time 12.96 Seconds
(without alignments)
15.078 Million cell updates/sec

Title: US-09-461-061A-1

Perfect score: 45

Sequence: 1 NNATFFFK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 48605

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	48.9	6	1	US-08-336-618-8
2	22	48.9	7	4	US-08-084-605B-14
3	21	46.7	4	4	US-08-669-304-5
4	21	46.7	4	4	US-08-669-304-12
5	20	44.4	7	1	US-08-302-449-11
6	20	44.4	7	5	PCT-US94-07430-11
7	20	44.4	8	4	US-08-160-604-7
8	19	42.2	4	4	US-09-177-249-143
9	19	42.2	6	2	US-08-282-980B-2
10	19	42.2	6	2	US-08-282-980B-3
11	19	42.2	6	2	US-08-282-980B-4
12	19	42.2	6	2	US-08-482-228-170
13	19	42.2	6	3	US-08-931-095-2
14	19	42.2	6	3	US-08-931-095-7
15	19	42.2	6	3	US-08-931-095-9
16	19	42.2	6	3	US-08-482-528-170
17	19	42.2	7	1	US-08-290-448A-82
18	19	42.2	7	1	US-08-290-448A-82
19	19	42.2	7	1	US-08-487-890A-81
20	19	42.2	7	1	US-08-175-069A-82
21	19	42.2	7	2	US-08-347-397-15
22	19	42.2	7	2	US-08-871-163-39
23	19	42.2	7	2	US-08-478-435-81
24	19	42.2	7	2	US-08-337-483-81
25	19	42.2	7	2	US-08-478-373-81
26	19	42.2	7	2	US-08-482-228-30
27	19	42.2	7	3	US-08-474-671-81

28 19 42.2 7 3 US-08-483-577A-81 Sequence 81, Appl
29 19 42.2 7 3 US-08-931-095-3 Sequence 3, Appl
30 19 42.2 7 3 US-08-482-528-30 Sequence 30, Appl
31 19 42.2 7 3 US-08-767-903-39 Sequence 39, Appl
32 19 42.2 7 4 US-08-897-438-81 Sequence 81, Appl
33 19 42.2 7 4 US-08-461-939B-82 Sequence 82, Appl
34 19 42.2 7 4 US-08-464-000-82 Sequence 82, Appl
35 19 42.2 7 4 US-08-637-654-81 Sequence 81, Appl
36 19 42.2 8 3 US-08-696-854B-10 Sequence 10, Appl
37 19 42.2 8 5 PCT-US91-02942-85 Sequence 85, Appl
38 18 40.0 5 1 US-07-924-753-6 Sequence 6, Appl
39 18 40.0 5 1 US-08-068-947-2 Sequence 2, Appl
40 18 40.0 5 4 US-09-066-481-23 Sequence 23, Appl
41 18 40.0 5 4 US-09-337-952-133 Sequence 133, App
42 18 40.0 5 4 US-09-521-650-133 Sequence 133, App
43 18 40.0 5 4 US-09-168-888-133 Sequence 133, App
44 18 40.0 6 2 US-08-377-432-37 Sequence 37, Appl
45 18 40.0 6 2 US-08-871-163-38 Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-08-336-618-8

; Sequence 8, Application US/08336618

; Patent No. 5763590

; GENERAL INFORMATION:

; APPLICANT: Peattie, Debra A.

; APPLICANT: Harding, Matthew W.

; APPLICANT: Livingston, David J.

; TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING

; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN

; TITLE OF INVENTION: CDNA

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/336,618

; FILING DATE: 09-NOV-1994

; PRIOR APPLICATION DATA:

; CLASSIFICATION: 435

; APPLICATION NUMBER: 07/963,325

; FILING DATE: 16-OCT-1992

; APPLICATION NUMBER: US 07/777,752

; FILING DATE: 11-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: VPI91-06A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-336-618-8

Query Match 48.9%; Score 22; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TYFK 8
| | | |
Db 2 TVYFK 6

RESULT 2
US-084-605B-14
; Sequence 14, Application US/09084605B
; Patent No. 6329501
; GENERAL INFORMATION:
; APPLICANT: Smith, Bruce F.
; APPLICANT: Samoilova, Tatiana
; TITLE OF INVENTION: Methods and Compositions for Targeting
; FILE OF INVENTION: Compounds to Muscle
; FILE REFERENCE: 5721-8
; CURRENT APPLICATION NUMBER: US/09/084,605B
; CURRENT FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phage display library peptides
US-084-605B-14

Query Match 48.9%; Score 22; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATFY 6
| | | |
Db 4 ATFY 7

RESULT 3
US-08-669-304-5
; Sequence 5, Application US/08669304
; Patent No. 6251626
; GENERAL INFORMATION:
; APPLICANT: Peter Stougaard
; APPLICANT: Ole Cai Hansen
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
; FILE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hunton & Williams
; STREET: 1900 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006-1109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,304
; FILING DATE: 12 July 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,910
; FILING DATE: 7 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stanislaus Aksman
; REGISTRATION NUMBER: 28,562
; REFERENCE/DOCKET NUMBER: 320.000003
; TELEPHONE: (202) 955-1926
; TELEFAX: (202) 778-2201
; TELEX: No. 6251626e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-669-304-12

NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: No. 6251626e
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-669-304-5

Query Match 46.7%; Score 21; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYFK 8
| | | |
Db 1 YYFK 4

RESULT 4
US-08-669-304-12
; Sequence 12, Application US/08669304
; Patent No. 6251626
; GENERAL INFORMATION:
; APPLICANT: Peter Stougaard
; APPLICANT: Ole Cai Hansen
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
; FILE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hunton & Williams
; STREET: 1900 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006-1109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,304
; FILING DATE: 12 July 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,910
; FILING DATE: 7 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stanislaus Aksman
; REGISTRATION NUMBER: 28,562
; REFERENCE/DOCKET NUMBER: 320.000003
; TELEPHONE: (202) 955-1926
; TELEFAX: (202) 778-2201
; TELEX: No. 6251626e
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-669-304-12

```
Query Match      46.7%; Score 21; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8
Db 1 YFK 4

RESULT 5
US-08-302-449-11
; Sequence 11, Application US/08302449
; Patent No. 5679635
; GENERAL INFORMATION:
; APPLICANT: Matalon, Reuben
; APPLICANT: Kaul, Rajinder
; APPLICANT: Cao, Guang Ping
; APPLICANT: Balamurugan, Kuppureddi
; APPLICANT: Michals-Matalon, Kimberlee
; TITLE OF INVENTION: Aspartoacylase Gene, Protein, and
; TITLE OF INVENTION: Methods of Screening for Mutations Associated with Canavan
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/128,020
; FILING DATE: 29-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07430
; FILING DATE: 05-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: SHUTT 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-302-449-11

Query Match      44.4%; Score 20; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFY 6
Db 2 NEAAVY 7

RESULT 6
US-08-160-604-7
; Sequence 7, Application US/08160604
; Patent No. 6232522
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; APPLICANT: James, Judith A.
; APPLICANT: Scofield, R. H.
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOG
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
```

```
PCT-US94-07430-11
; Sequence 11, Application PC/TUS9407430
; GENERAL INFORMATION:
; APPLICANT: Matalon, Reuben
; APPLICANT: Kaul, Rajinder
; APPLICANT: Cao, Guang Ping
; APPLICANT: Balamurugan, Kuppureddi
; APPLICANT: Michals-Matalon, Kimberlee
; TITLE OF INVENTION: Aspartoacylase Gene, Protein, and
; TITLE OF INVENTION: Methods of Screening for Mutations Associated with Canavan
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07430
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/128,020
; FILING DATE: 29-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: SHUTT 1P0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
PCT-US94-07430-11

Query Match      44.4%; Score 20; DB 5; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFY 6
Db 2 NEAAVY 7

RESULT 7
US-08-160-604-7
; Sequence 7, Application US/08160604
; Patent No. 6232522
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; APPLICANT: James, Judith A.
; APPLICANT: Scofield, R. H.
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOG
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
```

```
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160.604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-160-604-7

Query Match 44.4%; Score 20; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTYFK 8
   1 1
Db 1 TTYIK 5

RESULT 8
US-09-177-249-143
; Sequence 143, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Vagadari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 4
```

```
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; US-09-177-249-143

Query Match 42.2%; Score 19; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYF 7
   1 1 1
Db 2 FYF 4

RESULT 9
US-08-282-980B-2
; Sequence 2, Application US/08282980B
; Patent No. 5932189
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,980B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5932189nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..6
; OTHER INFORMATION: /label= cyclic
; OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
; OTHER INFORMATION: are linked by a covalent bond; the amino terminus
; OTHER INFORMATION: is substituted with a methyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..6
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The trp is in the D conformation; Xaa
; OTHER INFORMATION: is homocysteine."
; US-08-282-980B-2

Query Match 42.2%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```



```
Qy 5 FYFK 8
Db 1 FYWK 4

RESULT 10
US-08-282-980B-3
; Sequence 3, Application US/08282980B
; Patent No. 5932189
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,980B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5932189nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..6
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
; OTHER INFORMATION: are linked by a covalent bond; the amino terminus
; OTHER INFORMATION: is substituted with a methyl group."
; US-08-282-980B-3

Query Match 42.2%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8
Db 1 FYWK 4

RESULT 11
US-08-282-980B-4
; Sequence 4, Application US/08282980B
; Patent No. 5932189
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
```

```
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,980B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5932189nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..6
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Trp is in the D conformation; Xaa
; OTHER INFORMATION: is homocysteine."
; US-08-282-980B-4

Query Match 42.2%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8
Db 1 FYWK 4

RESULT 12
US-08-482-228-170
; Sequence 170, Application US/084822228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
```

STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-170

Query Match 42.2%; Score 19; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.7e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 TFYFK 8
Db 2 SFYFR 6

RESULT 13
US-08-931-095-2
Sequence 2, Application US/08931095
Patent No. 6017512
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: McBride, William
APPLICANT: Lister-James, John
TITLE OF INVENTION: Radiolabeled Peptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,095
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6017512nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
are linked by a covalent bond; the amino terminus
is substituted with a methyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The Trp is in the D conformation; Xaa
is homohomocysteine."
US-08-931-095-2

Query Match 42.2%; Score 19; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYFK 8
Db 1 FYWK 4

RESULT 14
US-08-931-095-7
Sequence 7, Application US/08931095
Patent No. 6017512
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: McBride, William
APPLICANT: Lister-James, John
TITLE OF INVENTION: Radiolabeled Peptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,095
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6017512nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site

```
; LOCATION: 1..6
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
; are linked by a covalent bond; the amino terminus
; OTHER INFORMATION: is substituted with a methyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Trp is in the D conformation."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= Chelator
; OTHER INFORMATION: /note= "A BAI chelator is covalently linked
; to the epsilon amino group of the Lys residue."
; US-08-931-095-7

Query Match 42.2%; Score 19; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FYFK 8
Db 1 FYWK 4

RESULT 15
US-08-931-095-9
; Sequence 9, Application US/08931095
; Patent No. 6017512
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Radiolabeled Peptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,095
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6017512nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..6
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
```

```
; OTHER INFORMATION: are linked by a covalent bond; the amino terminus
; OTHER INFORMATION: is substituted with a methyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Trp is in the D conformation."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /label= Chelator
; OTHER INFORMATION: /note= "A BAM chelator is covalently linked
; to the sidechain carboxyl group of Glu."
; US-08-931-095-9

Query Match 42.2%; Score 19; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FYFK 8
Db 1 FYWK 4

RESULT 16
US-08-482-528-170
; Sequence 170, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgeson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-528-170

Query Match 42.2%; Score 19; DB 3; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.7e+05;
```

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 TFEK 8
:||||
Db 2 SFYR 6

RESULT 17
US-08-290-448A-82
; Sequence 82, Application US/08290448A
; Patent No. 5676954
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,448A
; FILING DATE: August 15, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: May 29, 1990
; FILING DATE: March 17, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-448A-82

Query Match 42.2%; Score 19; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYF 7
|||
Db 5 FYF 7

RESULT 18
US-08-290-448A-82
; Sequence 82, Application US/08290448A
; Patent No. 5698204
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,448A
; FILING DATE: August 15, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: May 29, 1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: March 17, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-448A-82

Query Match 42.2%; Score 19; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYF 7
|||
Db 5 FYF 7

RESULT 19
US-08-487-890A-81
; Sequence 81, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175.116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148.968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-487-890A-81

Query Match 42.2%; Score 19; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NATFY 6
DB 2 NGAFY 6

RESULT 20
US-08-175-069A-82
; Sequence 82, Application US/08175069A
; Patent No. 5776761
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175.069A
; FILING DATE: December 29, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/529.951
; FILING DATE: May 29, 1990
; APPLICATION NUMBER: US 07/325.365
; FILING DATE: March 17, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-175-069A-82

Query Match 42.2%; Score 19; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYF 7
DB 5 FYF 7

Search completed: July 8, 2002, 11:38:46
Job time: 53 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein --protein search, using sw model

Run on: July 8, 2002, 11:41:19 ; Search time 24.98 Seconds
(without alignments)
46.160 Million cell updates/sec

Title: US-09-461-061A-2

Perfect score: 60

Sequence: 1 TLTHITKLNAE 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1579

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	36.7	11	2	TL7081
2	21	35.0	8	2	TL4906
3	21	35.0	10	2	D46285
4	19	31.7	10	2	A39745
5	17	28.3	11	2	PQ0733
6	17	28.3	12	2	PC4377
7	17	28.3	12	2	F84132
8	17	28.3	12	4	S49073
9	16	26.7	10	2	TL3976
10	16	26.7	10	2	TL4215
11	16	26.7	10	2	TL4223
12	16	26.7	10	2	A59173
13	15	25.0	7	2	S29735
14	15	25.0	9	2	JQ1202
15	15	25.0	9	2	PH0917
16	15	25.0	9	2	G85802
17	15	25.0	10	2	G53478
18	15	25.0	11	2	S58244
19	15	25.0	11	2	PC2330
20	15	25.0	12	2	B44818
21	15	25.0	12	2	PN0162
22	15	25.0	12	2	I77529
23	15	25.0	12	2	PT0255
24	14	23.3	7	2	A34026
25	14	23.3	7	2	PK0008
26	14	23.3	8	2	A47618
27	14	23.3	9	1	AKLQTM
28	14	23.3	9	2	S36898
29	14	23.3	9	2	PT0231

30 14 23.3 10 2 S23307
31 14 23.3 10 2 S23186
32 14 23.3 10 2 B33143
33 14 23.3 10 2 A33143
34 14 23.3 10 2 S59625
35 14 23.3 10 2 D61440
36 14 23.3 10 2 A61007
37 14 23.3 10 2 TL4219
38 14 23.3 11 2 PN0167
39 14 23.3 11 2 PU0034
40 14 23.3 12 2 S25485
41 14 23.3 12 2 PN0160
42 14 23.3 12 2 F61308
43 14 23.3 12 2 C20907
44 14 23.3 12 2 F20907
45 14 23.3 12 2 I57678

ALIGNMENTS

RESULT 1

TL7081

cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynocephalus raddei mitochondrion (frag
C:Species: mitochondrion Phrynocephalus raddei

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: TL7081

R:Macey, J.R.; Larson, A.; Anan'eva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial
A:Reference number: Z18674; MUID:97315309

A:Accession: TL7081

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <MAC>

A:Cross-references: EMBL:U82691; NID:g3603148; PID:g3603151; PIDN:AAC62302.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 36.7% Score 22; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLTH 4

Db 3 TLTH 6

RESULT 2

TL4906

hypothetical protein - parsley

C:Species: Petroselinum crispum (parsley)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: TL4906

R:Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weisshaar, B.

Plant Cell 6, 1607-1621, 1994

A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulat
A:Reference number: Z18259; MUID:95128172

A:Accession: TL4906

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <FEL>

A:Cross-references: EMBL:S75395; NID:g913201; PID:el94245

Query Match 35.0% Score 21; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTHIT 7

Db 1 MKHTLT 6 :||:|

RESULT 3

D46285
formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1996
C:Accession: D46285
R:Danielsson, O.; Jornvall, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992
A:Title: "Enzymogenesis": classical liver alcohol dehydrogenase origin from the glutathione
A:Reference number: A46285; MUID:93028441
A:Accession: D46285
A:status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <DAN>
A:Note: sequence extracted from NCBI backbone (NCBIP:116272)
C:Keywords: NAD; oxidoreductase

Query Match	35.0%;	Score 21;	DB 2;	Length 10;
Best Local Similarity	60.0%;	Pred. No. 7.5e+02;		

QY	2	LTHI	6
		:	111:
Db	4	VTHL	8

RESULT 4

A39745
 endo-glucosylceramidase activator II - *Rhodococcus* sp. (fragment)
 C:Species: *Rhodococcus* sp.
 C:Date: 30-Dec-1991 #sequence_revision 30 30-Sep-1993
 C:Accession: A39745
 R:Ito, M.; Ikegami, Y.; Yamagata, T.
 J. Biol. Chem. 266, 7919-7926, 1991.
 A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases. Evidence using these activator proteins.
 A:Reference number: A39745; MUID:91210321
 A:Accession: A39745
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <10>

Query Match 31.7%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4: Conservative 0; Mismatches 2; Indels

Qy	5	TITKLN	10
Db	3	TITPEN	8

RESULT 5

UNIDENTIFIED 6.0/15K PROTEIN [IMPORTED] - RICE (FRAGMENT)
 C:SPECIES: Oryza sativa (rice)
 C:DATE: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:ACCESSION: PQ0733
 R:KOMATSU, S.; KAJIWARA, H.; HIRANO, H.
 THEOR. APPL. GENET. 86, 935-942, 1993
 A:TITLE: A rice protein library; a data-file of rice proteins separated by two-dimensional
 A:REFERENCE NUMBER: PQ0696
 A:ACCESSION: PQ0733
 A:STATUS: preliminary
 A:MOLECULE TYPE: protein
 A:RESIDUES: 1-11 <KOM>

Query Match 28.3%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels

QY	4	HTI	6
Dp	1	HTI	3

RESULT

PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C/Accession: PC4377
R/Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A/Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the
A/Reference number: PC4371; MUID:97445086
A/Accession: PC4377
A/Molecule type: protein
A/Residues: 1-12 <SAR>
C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecul

Query Match 28.3%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	4	HTIT	7
		::	
Dp	5	HTVS	8

RESULT

hypothetical protein BH3862 [Imported] - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: F84132
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: F84132
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-12 <STO>
 A:Cross-references: GB:AP001520; GB:BA000004; NID:gl0176401; PIDN:BA07581.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3862

Query Match 28.3%; Score 17; DB 2; Length 12;
Best Local Similarity 25.0%; Pred. No. 5.3e+03;
Matches 2: Conservative 4: Mismatches 2: Indels 0: Gaps 0:

QY 2 LTHITKL 9
: : : : :
Db 1 MNYLLTKI 8

DECEMBER 1998

RESOLUT 6
 S49073
 Name shifted cytoadherence accessory protein HMW3 - Mycoplasma pneumoniae (fragment)
 N:Alternate names: H+-transporting ATP synthase (EC 3.6.1.34) alpha chain (misidentified)
 C:Species: Mycoplasma pneumoniae
 C:date: 28-Aug-1998 #sequence_revision 28-Aug-1998 #text_change 20-Apr-2000
 C:Accession: S49073
 R:Proft, T.; Herrmann, R.
 Mol. Microbiol. 13, 337-348, 1994
 A:title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae

A:Reference number: S49059; MUID:95075318

A:Accession: S49073

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-12 <PRO>

A:Cross-references: EMBL:232665; NID:9474163; PIDN:CAA83583.1; PID:9581348

A:Experimental source: clone D2-16

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

A:Note: the GenBank entry MPDASAL, release 106.0, translates the ATC codon, 1 in this re

C:Comment: The nucleotide sequence translated in an alternative reading frame is identic

C:Genetics:

A:Genetic code: SGC3

Query Match 28.3%; Score 17; DB 4; Length 12;

Best Local Similarity 80.0%; Pred. No. 5.3e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLTHT 5

||| 1

Db 3 TLTHT 7

RESULT 9

Tl3976

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment

C:Species: mitochondrion Cnemidophorus tigris

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: Tl3976

R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangement

A:Reference number: 217789; MUID:97153826

A:Accession: Tl3976

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71332; NID:9753236; PID:9753239; PIDN:AAB48274.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 26.7%; Score 16; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TITK 8

||| 1

Db 2 TITR 5

RESULT 10

Tl4215

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Varanus griseu mitochondrion (fragment)

C:Species: mitochondrion Varanus griseu

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: Tl4215

R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangement

A:Reference number: 217789; MUID:97153826

A:Accession: Tl4215

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71334; NID:93688056; PID:9753271; PIDN:AAD12669.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 26.7%; Score 16; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 6.7e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TITK 8

||| 1

Db 2 TITR 5

RESULT 11

Tl4223

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Xantusia vigilis mitochondrion (fragment)

C:Species: mitochondrion Xantusia vigilis

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: Tl4223

R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangem

A:Reference number: 217789; MUID:97153826

A:Accession: Tl4223

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71328; NID:9753276; PID:9753279; PIDN:AAB48291.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 26.7%; Score 16; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TITK 8

||| 1

Db 2 TITR 5

RESULT 12

A59173

nuclease Bh1 (EC 3.1.-.-) - Basidiobolus haptozporus (fragment)

C:Species: Basidiobolus haptozporus

C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: A59173

R:Desai, N.; Shankar, V.

submitted to the Protein Sequence Database, February 2000

A:Description: Single-strand-specific, guanylic acid preferential nuclease from Basid

A:Reference number: A59173

A:Accession: A59173

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <DES>

A:Note: extracellular, single-strand-specific nuclease

C:Keywords: hydrolase

Query Match

Best Local Similarity 26.7%; Score 16; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LTHFIT 7

||| 1

Db 4 LGHLLT 9

RESULT 13

S29735

polyphosphate--glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenre

C:Species: Propionibacterium freudenreichii subsp. shermanii

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C:Accession: S29735

R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A:Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermani*
A:Reference number: S29735; MUID:93143332
A:Accession: S29735

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <PHI>
C:Keywords: phosphotransferase

Query Match 25.0%; Score 15; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 THTI 6
| | :
Db 1 THVL 4

RESULT 14

J01202
leader peptide - *Pseudomonas* sp. plasmid R1033 transposon Tn1696

C:Species: *Pseudomonas* sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 12-Dec-1997
C:Accession: J01202
R:Stokes, H.W.; Hall, R.M.
Plasmid 26, 10-19, 1991

A:Title: Sequence analysis of the inducible chloramphenicol resistance determinant in the
A:Reference number: J01201; MUID:92052679

A:Accession: J01202
A:Molecule type: DNA
A:Residues: 1-9 <STO>

A:Cross-references: GB:M60454

C:Comment: This peptide is a potential translational attenuation signal for *cmlA* gene.
C:Genetics:

A:Genome: plasmid
C:Superfamily: unassigned leader peptides

Query Match 25.0%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TKLNAE 12
| | |
Db 3 TSKNAD 8

RESULT 15

PH0917

T-cell receptor beta chain V-D-J region (isolate 3) - rat (fragment)

C:Species: *Rattus norvegicus* (Norway rat)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0917

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857

A:Accession: PH0917

A:Molecule type: mRNA

A:Residues: 1-9 <SOL>

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 25.0%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NAE 12
| | |
Db 7 NAE 9

RESULT 16

G85802

hypothetical protein Z2947 [imported] - *Escherichia coli* (strain O157:H7, substrain E
C:Species: *Escherichia coli*

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: G85802

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: G85802

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-9 <STO>

A:Cross-references: GB:AE005174; NID:gl2515957; PIDN:AGS6883.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z2947

Query Match 25.0%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LTHITITKLN 10
| | | | |
Db 1 MTYTFMLSN 9

RESULT 17

S63478

dihydrolipoamide dehydrogenase (EC 1.8.1.4) beta chain E1 - *Pseudomonas aeruginosa* (f
N:Alternate names: branched-chain-oxoacid dehydrogenase chain E1

C:Species: *Pseudomonas aeruginosa*

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S63478

R:Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.

Eur. J. Biochem. 233, 828-836, 1995

A:Title: Purification of active E1-alpha(2)-beta(2) of *Pseudomonas putida* branched-ch
A:Reference number: S63475; MUID:96085147

A:Accession: S63478

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <HES>

C:Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase

Query Match 25.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 TITKL 9
| | :
Db 6 TVTSM 10

RESULT 18

S58244

pyrroloquinoline quinone synthase C - *Pseudomonas fluorescens* (fragment)

C:Species: *Pseudomonas fluorescens*

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999

C:Accession: S58244

R:Schneider, U.; Keel, C.; Defago, G.; Haas, D.

submitted to the EMBL Data Library, May 1995

A:Description: Tn5-directed cloning of *pqq* genes from *Pseudomonas fluorescens* CHA0: t
A:Reference number: S58239

A:Accession: S58244

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <SCH>

A:Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 25.0%; Score 15; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TITKLN 11
| | | | |
Db 2 TDTPLSA 8

RESULT 19

PC2330
cyclooligooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-255)
C:Species: Bacillus circulans
C:Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999
C:Accession: PC2330
R:Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A:Title: Purification and characterization of cyclooligooligosaccharide fructanotransferase
A:Reference number: PC2330; MUID:95201377
A:Accession: PC2330
A:Molecule type: protein
A:Residues: 1-11 <KUS>
C:Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 25.0%; Score 15; DB 2; Length 11;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 HTITKLN 12
| | | | |
Db 2 HLFYQMNQ 10

RESULT 20

B44818
extracellular lipase - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B44818
R:Gilbert, E.J.; Cornish, A.; Jones, C.W.
J. Gen. Microbiol. 137, 2223-2229, 1991
A:Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa
A:Reference number: A44818; MUID:92085040
A:Accession: B44818
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <GIL>
A:Experimental source: strain EF228
A>Note: sequence extracted from NCBI backbone (NCBIP:70393)

Query Match 25.0%; Score 15; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 THTTK 8
| | | | |
Db 1 THTTK 6

Search completed: July 8, 2002, 11:43:57
Job time: 158 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:43:29 ; Search time 13.1 Seconds
(without alignments)
35,468 Million cell updates/sec

Title: US-09-461-061A-2
Perfect score: 60
Sequence: 1 TLTHTITKLNAE 12

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 463

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	26.7	12	1 HCYB_MEGCR	Q10584 megathura c
2	15	25.0	11	1 PQOC_PSEFL	P55173 pseudomonas
3	15	25.0	12	1 PK4_PERFU	P82690 periplaneta
4	15	25.0	12	1 UH03_RAT	P56572 rattus norv
5	15	25.0	12	1 V25K_WSSV	P82004 white spot
6	14	23.3	8	1 FUSS_FUSSO	P81010 fusarium so
7	14	23.3	9	1 LMIP_LOCOMI	P31799 locusta mig
8	14	23.3	10	1 MALE_KLEPN	Q05564 klebsiella
9	14	23.3	10	1 PNEU_HUMAN	P22103 homo sapien
10	14	23.3	10	1 PNEU_RAT	P21996 rattus norv
11	14	23.3	10	1 SPL_HALRO	Q10997 halocynthia
12	14	23.3	10	1 TNKB_ONCMY	P28500 oncorhynch
13	14	23.3	10	1 UHA3_HUMAN	P40930 homo sapien
14	13	21.7	8	1 ACI_THUAL	P18691 thunnus alb
15	13	21.7	8	1 AKH_TABAT	P14595 tabanus atr
16	13	21.7	8	1 HPK1_PERAM	P04549 periplaneta
17	13	21.7	9	1 HPK2_PERAM	P82691 periplaneta
18	13	21.7	9	1 XYLA_STRSQ	P19149 streptomyce
19	13	21.7	10	1 AMPN_HELAM	P81731 helicoverpa
20	13	21.7	10	1 HTF2_CARMO	P11385 carausius m
21	13	21.7	10	1 HTF_TABAT	P14596 tabanus atr
22	13	21.7	12	1 PK4_PERAM	P82619 periplaneta
23	12	20.0	9	1 DCML_PSECF	P19913 pseudomonas
24	12	20.0	10	1 GON2_CHEPR	P80678 chelyosoma
25	12	20.0	11	1 TKNA_RANRI	P29207 rana ridibu
26	12	20.0	11	1 TKND_RANCA	P22691 rana catesb
27	12	20.0	12	1 V23K_WSSV	P82005 white spot
28	11	18.3	5	1 BIOB_CITFR	P12997 citrobacter
29	11	18.3	6	1 TRPI_PSEFU	P36414 pseudomonas
30	11	18.3	7	1 IGAO_DACDE	P06294 dactylium d
31	11	18.3	8	1 AKH_MELML	P25423 melolontha
32	11	18.3	8	1 HTF_TENMO	P25419 tenebrio mo
33	11	18.3	8	1 PUP_BRANA	P81707 brassica na

34	11	18.3	8	1 RPCH_PANBO	P08939 pandalus bo
35	11	18.3	9	1 MOSH_CLYJA	P19852 clypeaster
36	11	18.3	9	1 PGLR_DIAAB	P81179 diaprepes a
37	11	18.3	9	1 PTSP_BOMMO	P82003 bombyx mori
38	11	18.3	9	1 TAL1_PICJA	P17440 pichia jadi
39	11	18.3	9	1 TAL3_PICJA	P17441 pichia jadi
40	11	18.3	10	1 COX4_THUOB	P80971 thunnus obe
41	11	18.3	10	1 COXA_ONCMY	P80328 oncorhynch
42	11	18.3	10	1 FARP_MANSE	P18523 manduca sex
43	11	18.3	10	1 LABA_JATMU	P13270 jatrophia mu
44	11	18.3	10	1 Q2OG_COMTE	P80466 comamonas t
45	11	18.3	10	1 TNKB_RANRI	P29135 rana ridibu

ALIGNMENTS

RESULT 1
HCYB_MEGCR
ID HCYB_MEGCR STANDARD; PRT; 12 AA.
AC Q10584;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemocyanin B chain (KLH-B) (Fragment)
OS Megathura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Fissurellidae; Megathura.
OX NCBI_TaxID=55429;
RN [1]
RP SEQUENCE.
RX MEDLINE=96208935; PubMed=9829804;
RA Swardlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional
characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYPH OF MANY MOLLUSKS AND
ARTHROPODS.
CC -!- SUBUNIT: DIDEAMERS AND EXTENDED MULTIMERS.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: HEMOLYPH.
CC -!- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
protein for haptens and more recently in human vaccines and for
immunotherapy of bladder cancer.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
SUBFAMILY.
DR InterPro; IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Oxygen transport; Transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1345 MW; CBFBEAA44A432412 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 12;
Best Local Similarity 25.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TITKLNAE 12
| : : | :
Db 3 TVVRKNVD 10

RESULT 2
PQOC_PSEFL
ID PQOC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Fragment).

GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHA0;
RX MEDLINE=96064397; PubMed=8526497;
RA Schneider U., Keel C., Defago G., Haas D.;
RT "Tn5-directed cloning of pqg genes from Pseudomonas fluorescens CHA0:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)
CC BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER BACTERIAL PQQC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X87299; CAA60734.1; -.
KW PQQ.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46B4C5B73771 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TITKLA 11
| | | | |
Db 2 TDTPLSA 8

RESULT 3
PPK4_PERFU
ID PPK4_PERFU STANDARD; PRT; 12 AA.
AC P82690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (PEF-PK-4) (YAPRL-amide).
OS Periplaneta fuliginosa (Smokybrown cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=36977;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAA1 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LTHTI 6
| | | :
Db 3 LSHDV 7

RESULT 4
UH03_RAT
ID UH03_RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=WISTAR; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.3, ITS MW IS: 28 kDa.
FT UNSURE 2 2
FT NON_TER 9 9
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 HTITKL 9
| | | :
Db 3 HTKIKV 8

RESULT 5
V25K_WSSV
ID V25K_WSSV STANDARD; PRT; 12 AA.
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; Unassigned viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 12;
Best Local Similarity 30.0%; Pred. No. 4e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 LTHFITKLA 11

Db 3 LSFTLSVTA 12

RESULT 6
FUSO_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s 13596* (Fragment).
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Haematonectria.
OX NCBI_TaxID=109625;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON_TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+05;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTHTI 6
Db 3 MSHNV 7

RESULT 7
LMIP_LOCMI STANDARD; PRT; 9 AA.
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyoinhibiting peptide (LOM-MIP).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OX Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria".
RL Regul. Pept. 36:111-119(1991).
CC -!- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND OVIDUCT.
CC -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBESOPHAGEAL GANGLION.
DR PIR: A60065; AKLOIM.
KW Amidation; Neuropeptide.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LNA 11
Db 5 LNA 7

RESULT 8
MALE_KLEPN STANDARD; PRT; 10 AA.
AC Q05564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein) (MMBP) (Fragment).
DE MALE.
GN MALE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-5P14 / KAY2026;
RX MEDLINE=93211295; PubMed=8459773;
RA Bachelier S., Perrin D., Hofnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMES) are present in the genome of Klebsiella".
RL Mol. Microbiol. 7:537-544(1993).
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X68329; CAA48406.1; -.
DR InterPro; IPR000567; SBP_bac_1.
DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ITK 8
Db 8 ITK 10

RESULT 9
PNEU_HUMAN STANDARD; PRT; 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KLNA 11
||:|
Db 5 KLDA 8

RESULT 10
PNEU_RAT
ID PNEU_RAT STANDARD; PRT; 10 AA.
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
Regul. Pept. 30:77-87(1990).
RL "Pneumadin: a new lung peptide which triggers antidiuresis.";
CC -!- FUNCTION: THIS ANTIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KLNA 11
||:|
Db 5 KLDA 8

RESULT 11
SPI_HALRO
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (fragment).
OS Halocynthia roretzi (Sea squirt).
CC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=96321313; PubMed=8759295;
RA Shiohikura F., Abe T., Ohtake S.-I., Tanaka K.;
"Purification and characterization of a 58,000-Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halocynthia
roretzi.";

RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TKLNAE 12
||:|
Db 1 TKDGE 6

RESULT 12
TKNB_ONCMY
ID TKNB_ONCMY STANDARD; PRT; 10 AA.
AC P28500;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurokinin A (Substance K) (Neurokinin I).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
OS Gadus morhua (Atlantic cod).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022, 8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
"Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S23186; S23186.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KLNA 11
||:|
Db 2 KINS 5

RESULT 13
UHA3_HUMAN
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).


```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RL 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TIT 7
Db 5 TIT 7

RESULT 14
ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RL muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TH 4
Db 2 TH 3

RESULT 15
AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Adipokinetic hormone (AKH) (Diptera corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;

```

```

OC Tabanidae; Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.;
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuro peptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTHT 5
Db 2 LTFT 5

RESULT 16
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (PEA-CAH-II) (LED-CC-II) (Hypertrehalosemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=95046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RL cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;

```

```

RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RL beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RL Gromphadorhina portentos, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Sevler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RECH FAMILY.
DR PIR; A05170; A05170.
DR PIR; S08996; S08996.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LTHT 5
DB 2 LTFT 5

RESULT 17
PPK1_PERAM
ID PPK1_PERAM STANDARD; PRT; 9 AA.
AC P82691;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Pea-PK-1) (FXPR1-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RL retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPR1amides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- TISSUE SPECTROMETRY: MW=1010.4; METHOD=WALDI.

```

```

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HT 5
DB 1 HT 2

RESULT 18
XYLA_STRSQ
ID XYLA_STRSQ STANDARD; PRT; 9 AA.
AC P19149;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.
OS Streptomyces sp. (strain NCL 82-5-1).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RX MEDLINE=88326335; PubMed=3415697;
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT "Purification and characterisation of glucose (xylose) isomerase from
RT Chaetia sp. (NCL 82-5-1).";
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC -!- FUNCTION: INVOLVED IN D-XYLOSE CATABOLISM.
CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -!- COFACTOR: Magnesium; binds 2 ions per subunit (Potential).
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR PIR; A31576; A31576.
DR InterPro; IPR001998; Xylose_isom.
DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HT 5
DB 7 HT 8

RESULT 19
AMPN_HELAM
ID AMPN_HELAM STANDARD; PRT; 10 AA.
AC P81731;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Aminopeptidase N (EC 3.4.11.2) (Fragment).
OS Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.

```

```

OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE.
RC TISSUP-Midgut;
RA Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatpar H.S.;
RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC
RT toxin from Helicoverpa armigera";
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
CC -1- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid,
CC preferably a neutral or hydrophobic one, from a polypeptide.
CC Aminocacyl-arylamides are poor substrates.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
CC PROTEOLYTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.
DR InterPro: IPR00130; Zn_MTPeptidse.
DR PROSITE: PS00142; ZINC_PROTEASE; PARTIAL.
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
FT NON_TER 10
SQ .SEQUENCE 10 AA; 1093 MW; 05042EB87B11F1BB CRC64;

Query Match 21.7%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TH 4
Db 4 TH 5

RESULT 20
HTF2_CARMO
ID HTF2_CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemiidae;
OC Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RC SPECIES=C.morosus; TISSUP-Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiacum of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=E.tiaratum; TISSUP-Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.morosus; TISSUE-Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiacum.";

```

```

RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=HPLC.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S07157; S07157.
DR PIR: S09138; S09138.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

```

```

Query Match 21.7%; Score 13; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 LTHT 5
Db 2 LTFT 5

```

```

Search completed: July 8, 2002, 11:48:58
Job time: 329 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:43:26 ; Search time 21.49 Seconds
(without alignments)
13.639 Million cell updates/sec

Title: US-09-461-061A-3

Perfect score: 56

Sequence: 1 IDNVKARQVV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 83765

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	42.9	12	1	US-07-995-657-7
2	24	42.9	12	1	US-08-474-587-7
3	23	41.1	8	4	US-08-160-604-83
4	23	41.1	8	4	US-08-160-604-84
5	23	41.1	8	4	US-08-160-604-85
6	23	41.1	9	2	US-08-908-526-6
7	23	41.1	9	3	US-08-159-339A-127
8	23	41.1	10	2	US-08-428-257A-6
9	23	41.1	11	1	US-08-378-761A-68
10	23	41.1	11	1	US-08-485-286-68
11	23	41.1	12	2	US-08-908-526-2
12	22	39.3	8	4	US-08-160-604-86
13	22	39.3	9	1	US-08-321-668-10
14	22	39.3	9	1	US-08-837-941-10
15	22	39.3	11	4	US-08-647-405B-6
16	22	39.3	12	1	US-08-321-668-15
17	22	39.3	12	1	US-08-837-941-15
18	21	37.5	9	1	US-08-594-447-42
19	21	37.5	9	1	US-08-541-964-41
20	21	37.5	9	2	US-08-665-647-56
21	21	37.5	10	1	US-08-166-195A-45
22	21	37.5	10	2	US-08-436-772-45
23	21	37.5	10	2	US-08-436-883B-45
24	21	37.5	11	2	US-08-762-695-1
25	21	37.5	11	4	US-08-647-405B-7
26	21	37.5	12	1	US-08-313-681A-13
27	21	37.5	12	1	US-08-321-668-16

28	21	37.5	12	1	US-08-321-668-17
29	21	37.5	12	1	US-08-321-668-18
30	21	37.5	12	1	US-08-321-668-19
31	21	37.5	12	1	US-08-837-941-16
32	21	37.5	12	1	US-08-837-941-17
33	21	37.5	12	1	US-08-837-941-18
34	21	37.5	12	1	US-08-837-941-19
35	21	37.5	12	3	US-09-322-911-13
36	21	37.5	12	4	US-08-687-590-4
37	20	35.7	5	4	US-09-187-859-3201
38	20	35.7	6	4	US-09-187-859-3711
39	20	35.7	7	4	US-09-187-859-3712
40	20	35.7	7	4	US-09-187-859-3714
41	20	35.7	8	4	US-08-160-604-82
42	20	35.7	8	4	US-09-187-859-3715
43	20	35.7	8	4	US-09-187-859-3717
44	20	35.7	9	2	US-08-704-655-3
45	20	35.7	9	3	US-08-159-339A-128

ALIGNMENTS

RESULT 1
US-07-995-657-7
; Sequence 7, Application US/07995657
; Patent No. 5443974
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase cDNA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07995,657
; FILING DATE: 19921211
; FILING DATE: C) CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GEIGER, KATHLEEN W.
; REGISTRATION NUMBER: 35,880
; REFERENCE/DOCKET NUMBER: BB_1022-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-995-657-7

Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 3201, Ap
Sequence 3711, Ap
Sequence 3712, Ap
Sequence 3714, Ap
Sequence 82, Appl
Sequence 3715, Ap
Sequence 3717, Ap
Sequence 3, Appl
Sequence 128, App

Query Match 42.9%; Score 24; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNVK 6
:::|
Db 3 VENIKK 8

RESULT 2
US-08-474-587-7
; Sequence 7, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez_Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase cDNA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,587

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: SIEGELL, BARBARA C.

REGISTRATION NUMBER: 30,684

REFERENCE/DOCKET NUMBER: BB_1022-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4931

TELEFAX: 302-773-0164

TELEX: 835420

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-474-587-7

Query Match 42.9%; Score 24; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDNVK 6
:::|
Db 3 VENIKK 8

RESULT 3
US-08-160-604-83
; Sequence 83, Application US/08160604
; Patent No. 6232522

GENERAL INFORMATION:
APPLICANT: Harley, John
APPLICANT: James, Judith A.
APPLICANT: Scofield, R. H.
TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,604
FILING DATE: 30-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,819
FILING DATE: 13-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,205
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,947
FILING DATE: 31-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-160-604-83

Query Match 41.1%; Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VKKARV 9
:||||
Db 3 LKKARI 8

RESULT 4
US-08-160-604-84
; Sequence 84, Application US/08160604
; Patent No. 6232522

GENERAL INFORMATION:
APPLICANT: Harley, John
APPLICANT: James, Judith A.
APPLICANT: Scofield, R. H.
TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,604
FILING DATE: 30-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,819
FILING DATE: 13-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,205
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,947
FILING DATE: 31-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR114CIP(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-160-604-84

Query Match 41.1% Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0;

Qy 4 VKKARV 9
:||||:
Db 2 LKKARI 7

RESULT 5
US-08-160-604-85
Sequence 85, Application US/08160604
Patent No. 6232522
GENERAL INFORMATION:
APPLICANT: Harley, John
APPLICANT: James, Judith A.
APPLICANT: Scofield, R. H.
TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,604
FILING DATE: 30-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,819
FILING DATE: 13-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,205
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,947
FILING DATE: 31-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR114CIP(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-160-604-85

Query Match 41.1% Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0;

Qy 4 VKKARV 9
:||||:
Db 1 LKKARI 6

RESULT 6
US-08-908-526-6
Sequence 6, Application US/08908526
Patent No. 5876730
GENERAL INFORMATION:
APPLICANT: Brigstock, David R.
APPLICANT: Harding, Paul H.
TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,526
FILING DATE: 07-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A., Ph.D.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 08766/003002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-526-6

Query Match 41.1% Score 23; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.7e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVKKAR 8
:|:|:
DB 2 ENIKKGK 8

RESULT 7

US-08-159-339A-127
Sequence 127, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-127

Query Match 41.1% Score 23; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDNVKK 6
:|:|:
DB 3 IDNVYK 8

RESULT 8

US-08-428-257A-6
Sequence 6, Application US/08428257A
Patent No. 5885808

GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.

TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-6

Query Match 41.1% Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 VKKRVQV 11
:|:|:
DB 2 LKTKVQL 9

RESULT 9

US-08-378-761A-68
Sequence 68, Application US/08378761A
Patent No. 5635384

GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,761A
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-378-761A-68

Query Match 41.1%; Score 23; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKARV 9
| | | | |
DB 3 KKARV 7

RESULT 10
US-08-485-286-68
; Sequence 68, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 68:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-485-286-68

Query Match 41.1%; Score 23; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKARV 9
| | | | |
DB 3 KKARV 7

RESULT 11
US-08-908-526-2
; Sequence 2, Application US/08908526
; Patent No. 5876730
; GENERAL INFORMATION:
; APPLICANT: Brigstock, David R.
; APPLICANT: Harding, Paul H.
; TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,526
; FILING DATE: 07-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A., Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08766/003002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-908-526-2

Query Match 41.1%; Score 23; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNVKKAR 8
: | : | :
DB 1 ENIKKGK 7

RESULT 12
US-08-160-604-86

```
; Sequence 86, Application US/08160604
; Patent No. 6232522
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; APPLICANT: James, Judith A.
; APPLICANT: Scofield, R. H.
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-160-604-86

Query Match 39.3%; Score 22; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKAR 9
| | | |
Db 1 KKRI 5

RESULT 13
US-08-321-668-10
; Sequence 10, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE

; Sequence 86, Application US/08160604
; Patent No. 6232522
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; APPLICANT: James, Judith A.
; APPLICANT: Scofield, R. H.
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-160-604-86
```

```
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= hu p55 TNF-R mutant
; OTHER INFORMATION: construct 175-179
; US-08-321-668-10

Query Match 39.3%; Score 22; DB 1; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDNVKRV 9
| | | | |
Db 1 IENVKGV 9

RESULT 14
US-08-837-941-10
; Sequence 10, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/837,941
;; FILING DATE: 28-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/321,668
;; FILING DATE: 12-OCT-1994
;; APPLICATION NUMBER: IL 107268
;; FILING DATE: 12-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: WALLACH-13
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: /note= hu p55 TNF-R mutant
;; OTHER INFORMATION: construct 175-179
US-08-837-941-10

Query Match 39.3%; Score 22; DB 1; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDNVKKARV 9
|:|:|:|
Db 1 IENVKGTIV 9

RESULT 15
US-08-647-405B-6
;; Sequence 6, Application US/08647405B
;; Patent No. 6228654
;; GENERAL INFORMATION:
;; APPLICANT: Chait, Brian T.
;; APPLICANT: Zhao, Yingming
;; APPLICANT: Kent, Stephen B.H.
;; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
;; FILE REFERENCE: Oligosaccharides
;; CURRENT APPLICATION NUMBER: US/08/647,405B
;; CURRENT FILING DATE: 1996-05-09
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:..Related to
;; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-6

Query Match 39.3%; Score 22; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DNVKKAR 8
|:|:|:
Db 5 DTVEKAK 11

RESULT 16
US-08-321-668-15
;; Sequence 15, Application US/08321668
;; Patent No. 5665859
;; GENERAL INFORMATION:
;; APPLICANT: WALLACH, David
;; APPLICANT: BRAKEBUSCH, Cord
;; APPLICANT: VAREFOLOMEEV, Eugene
;; APPLICANT: BATKIN, Michael
;; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
;; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;; NUMBER OF SEQUENCES: 42
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/321,668
;; FILING DATE: 12-OCT-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 107268
;; FILING DATE: 12-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: WALLACH-13
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: /note= hu p55 TNF-R mutant
;; OTHER INFORMATION: construct 175-176
US-08-321-668-15

Query Match 39.3%; Score 22; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDNVKK 6
|:|:|:
Db 1 IENVKE 6

RESULT 17
US-08-837-941-15
;; Sequence 15, Application US/08837941
;; Patent No. 5766917
;; GENERAL INFORMATION:
;; APPLICANT: WALLACH, David
;; APPLICANT: BRAKEBUSCH, Cord
;; APPLICANT: VAREFOLOMEEV, Eugene
;; APPLICANT: BATKIN, Michael
;; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
;; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;; NUMBER OF SEQUENCES: 42

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;;
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/837,941
;; FILING DATE: 28-APR-1997
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/321,668
;; FILING DATE: 12-OCT-1994
;; APPLICATION NUMBER: IL 107268
;; FILING DATE: 12-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: WALLACH-13
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;;
;; OTHER INFORMATION: /note= hu p55 TNF-R mutant
;; OTHER INFORMATION: construct 175-176
US-08-837-941-15

Query Match 39.3%; Score 22; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDNVKK 6
|:|:|:
Db 1 IENVKE 6

RESULT 18
US-08-594-447-42
; Sequence 42, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PC-THETA, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/594,447
;; FILING DATE: 31-JAN-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 22550-20025.24
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 822-0168
;; TELEX: 90-4030 MRSNFOERSWSH
;; INFORMATION FOR SEQ ID NO: 42:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..9
;; OTHER INFORMATION: /label= epsilon-V3-3
US-08-594-447-42

Query Match 37.5%; Score 21; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNVKKA 7
|:|:|:
Db 2 NNIRKA 7

RESULT 19
US-08-541-964-41
; Sequence 41, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..9
OTHER INFORMATION: /label= epsilon-V3-3
US-08-541-964-41

Query Match 37.5%; Score 21; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNVKKA 7
Db 2 NNIRKA 7

RESULT 20
US-08-665-647-56
; Sequence 56, Application US/08665647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit
; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /label= epsilon-V3-3
US-08-665-647-56

Query Match 37.5%; Score 21; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNVKKA 7
Db 2 NNIRKA 7

Search completed: July 8, 2002, 11:43:26
Job time: 148 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:38:48 ; Search time 10.15 Seconds
(without alignments)
30.518 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFFYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	40.0	8	1 UPAA_HUMAN	P30096 homo sapien
2	16	35.6	8	1 LCK8_LEUMA	P19990 leucophaea
3	15	33.3	5	1 PAP2_PARMA	P81864 pardachirus
4	14	31.1	4	1 FEKA_ATEL	P58705 anthopleura
5	14	31.1	8	1 LCK4_LEUMA	P21143 leucophaea
6	13	28.9	4	1 FYRI_ATEL	P58706 anthopleura
7	12	26.7	5	1 TPIS_CANFA	P54714 canis famil
8	12	26.7	8	1 NPB_BOVIN	P15507 bos taurus
9	11	24.4	6	1 FARP_MONEX	P41966 moniezia ex
10	11	24.4	7	1 FARI_PROCL	P38499 procambarus
11	11	24.4	8	1 ARH_TABAT	P4595 tabanus atr
12	11	24.4	8	1 COXG_RAT	P80430 rattus norv
13	11	24.4	8	1 FAR4_HOMAM	P41487 homarus ame
14	11	24.4	8	1 HTF2_PERAM	P04549 periplaneta
15	11	24.4	8	1 RS1_ERWCH	P37985 erwinia chr
16	11	24.4	8	1 UC26_MAIZE	P80632 zea mays (m
17	10	22.2	5	1 UC22_MAIZE	P80628 zea mays (m
18	10	22.2	6	1 TMOF_SARBU	P41495 sarcophaga
19	10	22.2	6	1 UN06_CLOPA	P81351 clostridium
20	10	22.2	7	1 CCF1_ENTFA	P20104 enterococcu
21	10	22.2	7	1 UN06_PINPS	P81675 pinus pinas
22	10	22.2	7	1 LCK6_LEUMA	P19988 leucophaea
23	9	20.0	4	1 FAR3_HIRME	P42562 hirudo medi
24	9	20.0	4	1 FAR4_HIRME	P42563 hirudo medi
25	9	20.0	5	1 FARP_ARTTR	P41853 artiopesthi
26	9	20.0	5	1 RE11_LITRU	P82070 litoria rub
27	9	20.0	5	1 RE21_LITRU	P82071 litoria rub
28	9	20.0	5	1 RE31_LITRU	P82072 litoria rub
29	9	20.0	5	1 RE32_LITRU	P19991 acheta dome
30	9	20.0	5	1 SUGA_ACHDO	P19991 acheta dome
31	9	20.0	7	1 CIA_ENTFA	P11932 enterococcu
32	9	20.0	7	1 FAR2_ASCSU	P31890 ascaris suu
33	9	20.0	7	1 FAR3_HAECO	P81298 haemonchus

```
34 9 20.0 7 1 FAR3_PANRE P41874 panagrellus
35 9 20.0 7 1 FAR5_HIRWE P42564 hirudo medi
36 8 1 ARHG_GRYBI P14086 gryllus bim
37 9 20.0 8 1 AKH_LITAU P25418 libellula a
38 9 20.0 8 1 B44K_PORGI P81886 porphyromon
39 8 17.8 6 1 OVM_LEPDE P42985 leptinotars
40 8 17.8 7 1 ALL5_CARMA P81808 carcinus ma
41 8 17.8 7 1 CHOX_ALCSP P16101 alcaligenes
42 8 17.8 7 1 HY7_PIG P01153 sus scrofa
43 8 17.8 7 1 TY51_LITRU P82065 litoria rub
44 8 17.8 8 1 ALL7_CARMA P81809 carcinus ma
45 8 17.8 8 1 LPMS_STAEP P23211 staphylococ
```

ALIGNMENTS

```
RESULT 1
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 5 F -> P.
FT VARIANT 5 5 /FTId=VAR_000004.
SQ NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;
```

Query Match 40.0%; Score 18; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TFF 6
DB 4 TFF 6

```
RESULT 2
LCK8_LEUMA
ID LCK8_LEUMA STANDARD; PRT; 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
```

RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0318; JS0318
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 35.6%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+05; 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 3 ATFF 6
Db 2 ADFY 5

RESULT 3
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 33.3%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYF 7
Db 2 FFF 4

RESULT 4
FFKA_ANTEL
ID FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actinidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RN FUNCTION.
RX PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 31.1%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YFK 8
Db 1 FFK 3

RESULT 5
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 31.1%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+05; 0; Gaps 0;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFY 6


```
Db 1 DASPH 5
:|:|:
RESULT 6
FYRI_ATEL
ID FYRI_ATEL STANDARD; PRT; 4 AA.
AC P58706;
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX PubMed=1821096;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its
RT des-phenylactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
RN FUNCTION.
RX PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RA "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 28.9%; Score 13; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FY 6
| |
Db 1 FY 2

RESULT 7
TPIS_CANFA
ID TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TP11.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
RC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of

dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000652; Trioseph_isomerase.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 26.7%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NN 2
| |
Db 4 NN 5

RESULT 8
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Brain;
RC MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT SIMILAR 5 8
FT MOD_RES 5 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 26.7%; Score 12; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. le+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FYFK 8
| | |
Db 1 FLFQ 4

RESULT 9
FARP_MONEX
ID FARP_MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRFamide-like neuropeptide GNFFRF-amide.
```

OS Monilezia expansa (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
 OC Rhadithophora; Eulecithophora; Revertospermata; Mediofusata;
 OC Neodermata; Cestoda; Eucestoda; Cyclophyllidae; Anoplocephalidae;
 OC Monilezia.
 OX NCBI_TaxID=28841;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93312289; PubMed=8323531;
 RA Maule A.G.; Shaw C.; Halton D.W.; Thim L.;
 RT "GNFRamide: a novel FMRFamide-immunoreactive peptide isolated from
 the sheep tapeworm, Monilezia expansa.";
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 24.4%; Score 11; DB 1; Length 6;
 Best Local Similarity 33.3%; Pred. No. 1e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YFK 8
 Db 3 PFR 5

RESULT 10

ID FARI_PROCL STANDARD; PRT; 7 AA.
 AC P38499;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog NPL.
 OS Procamburus clarkii (Red swamp crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procamburus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.

TISSUE=Pericardial Organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J.; Orchard I.; Tebruge V.; Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 24.4%; Score 11; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NATF 5
 Db 1 NRNF 4

RESULT 11

AKH_TABAT
 ID AKH_TABAT STANDARD; PRT; 8 AA.
 AC P14595;

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor 1)
 DE (DCC 1).
 DE Tabanus atratus (Horse fly).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
 OC Tabanidae; Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H.; Raina A.K.; Riley C.T.; Fraser B.A.; Nachman R.J.;
 RA Vogel V.W.; Zhang Y.-S.; Hayes D.K.;
 RT "Primary structure of two neuro peptide hormones with adipokinetic and
 hypotrehalosemic activity isolated from the corpora cardiaca of horse
 flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RFCH FAMILY.
 DR PIR; A33995; A33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 24.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TF 5
 Db 3 TF 4

RESULT 12

ID COXG_RAT STANDARD; PRT; 8 AA.
 AC P80430;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Cytochrome c oxidase polypeptide V1b (BC 1.9.3.1) (AED) (Fragment).
 GN COX6B.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.

STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=9534529; PubMed=7601105;
 RA Schaeffer H.; Noack H.; Halangk W.; Brandt U.; von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 amino-terminal sequences suggest identity of the fetal heart and the
 adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- FUNCTION: THIS PROTEIN MAY BE ONE OF THE HEME-BINDING SUBUNITS OF
 THE OXIDASE.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 KW Oxidoreductase; Mitochondrion.

```

FT  NON_TER      1      1
FT  NON_TER      8      8
SQ  SEQUENCE     8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

Query Match      24.4%; Score 11; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1  NATF 6
    |  |
Db  2  NXLDHF 7

RESULT 13
ID  FAR4_HOMAM  STANDARD; PRT; 8 AA.
AC  P41487;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FMRamide-like neuropeptide 4 (FLI 4) (F1).
OS  Homarus americanus (American lobster).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC  Nephropoidea; Nephropidae; Homarus.
OX  NCBI_TaxID=6706;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Pericardial organs;
RX  MEDLINE=88116164; PubMed=3429714;
RA  Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT  "Purification and characterization of FMRamide-like immunoreactive
RT  substances from the lobster nervous system: isolation and sequence
RT  analysis of two closely related peptides.";
RL  J. Comp. Neurol. 266:16-26(1987).
CC  -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC  NEUROMUSCULAR JUNCTIONS.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC  FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD_RES      8      8
SQ  SEQUENCE     8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match      24.4%; Score 11; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  NATF 5
    |  |
Db  2  NRNF 5

RESULT 14
ID  HTF2_PERAM  STANDARD; PRT; 8 AA.
AC  P04549;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  01-FEB-1994 (Rel. 28, Last annotation update)
DE  Hypertrehalosemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE  (Pea-CAH-II) (Ileu-CC-II) (Hypertrehalosemic neuropeptide II).
OS  Periplaneta americana (American cockroach),
OS  Leptinotarsa decemlineata (Colorado potato beetle), and
OS  Blatta orientalis (Oriental cockroach).
OC  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC  Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC  Blattodea; Blattidae; Periplaneta.
OX  NCBI_TaxID=6978, 7539, 6976;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=P.americana;

```

```

RX  MEDLINE=85046530; PubMed=6548628;
RA  Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA  Rinehart K.L. Jr.;
RT  "Structures of two cockroach neuropeptides assigned by fast atom
RT  bombardment mass spectrometry.";
RL  Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN  [2]
RP  SEQUENCE.
RC  SPECIES=P.americana;
RX  MEDLINE=84298179; PubMed=6591205;
RA  Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA  Miller C.A., Schooley D.A.;
RT  "Isolation and primary structure of two peptides with
RT  cardioacceleratory and hyperglycemic activity from the corpora
RT  cardiaca of Periplaneta americana.";
RL  Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN  [3]
RP  SEQUENCE.
RC  SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX  MEDLINE=90160053; PubMed=2576128;
RA  Gaede G., Kellner R.;
RT  "The metabolic neuropeptides of the corpus cardiacum from the potato
RT  beetle and the American cockroach are identical.";
RL  Peptides 10:1287-1289(1989).
RN  [4]
RP  SEQUENCE.
RC  SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX  MEDLINE=90253659; PubMed=2340112;
RA  Gaede G., Rinehart K.L. Jr.;
RT  "Primary structures of hypertrehalosemic neuropeptides isolated from
RT  the corpora cardiaca of the cockroaches Leucophaea maderae,
RT  Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT  and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT  atom bombardment mass spectrometry.";
RL  Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC  -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC  ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH OF INSECTS.
CC  -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR  PIR; A05170; A05170.
DR  PIR; S08996; S08996.
DR  PIR; B4960; B4960.
DR  PIR; B49823; B49823.
DR  InterPro; IPR002047; AKH.
DR  PROSITE; PS00256; AKH; 1.
KW  Neuropeptide; Amidation.
FT  MOD_RES      1      1
FT  MOD_RES      8      8
SQ  SEQUENCE     8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match      24.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  TF 5
    |  |
Db  3  TF 4

RESULT 15
ID  RSL_ERWCH  STANDARD; PRT; 8 AA.
AC  P37985;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  30S ribosomal protein S1 (Fragment).
OS  RPSA.
OS  Erwinia chrysanthemi.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Pectobacterium.
OX  NCBI_TaxID=556;

```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=3937;
RA  Doullie A., Toussaint A., Faelen M.;
RL  Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC  INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC  SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X74750; CAA52769.1; -
DR  PIR; S37141; S37141.
KW  Ribosomal protein; Repeat; RNA-binding.
FT  NON_TER 1
SQ  SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match      24.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 FK 8
DB  2 FK 3

RESULT 16
UC26_MAIZE
ID  UC26_MAIZE STANDARD; PRT; 8 AA.
AC  P80632;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE  (Fragment).
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC  Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
RT  genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR  Maize-2DPAGE; P80632; COLEOPTILE.
DR  MaizedB; 123954; -
DR  MaizedB; 123954; -
FT  NON_TER 1
FT  NON_TER 8
SQ  SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

```

```

Query Match      24.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 FK 8
DB  7 FK 8

```

```

RESULT 17
UC22_MAIZE
ID  UC22_MAIZE STANDARD; PRT; 5 AA.
AC  P80628;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE  (Fragment).
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC  Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
RT  genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR  Maize-2DPAGE; P80628; COLEOPTILE.
DR  MaizedB; 123954; -
DR  MaizedB; 123954; -
FT  NON_TER 1
FT  NON_TER 5
SQ  SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

```

```

Query Match      22.2%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  6 YFK 8
DB  2 FFE 4

```

```

RESULT 18
TM0F_SARBU
ID  TM0F_SARBU STANDARD; PRT; 6 AA.
AC  P41495;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  Trypsin-modulating oostatic factor (TM0F).
OS  Sarcophaga bullata (grey flesh fly) (Neobellieria bullata).
OC  Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Oestroidea; Sarcophagidae; Sarcophaga.
OX  NCBI_TaxID=7385;
RN  [1]
RP  SEQUENCE, AND SYNTHESIS.
RC  TISSUE=Ovary;
RX  MEDLINE=94211930; PubMed=8159807;
RA  Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA  de Loof A.;
RT  "Sequencing and characterization of trypsin modulating oostatic
RT  factor (TM0F) from the ovaries of the grey fleshfly, Neobellieria
RT  (Sarcophaga) bullata.";
RL  Regul. Pept. 50:61-72(1994).
CC  -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC  IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC  CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
CC  DEVELOPMENT.
CC  -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC  EPITHELIUM AFTER A BLOOD MEAL.
KW  Hormone.
SQ  SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

```

Query Match 22.2%; Score 10; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NAT 4
| |
Db 1 NPT 3

RESULT 19
UN06_CLOPA
ID UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein Cp 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_taxid=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
FT NON_TER 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 22.2%; Score 10; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNA 3
| |
Db 2 NTA 4

RESULT 20
CCFL_ENTFA
ID CCFL_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -|- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR: A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 22.2%; Score 10; DB 1; Length 7;

Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TFFV 7
| |
Db 3 TLVF 6

Search completed: July 8, 2002, 11:42:02
Job time: 194 sec


```
ID Q40530 PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE P20 N WITH A LEADER PEPTIDE.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C6 CRC64;

Query Match 35.6%; Score 16; DB 10; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8
Db 2 FFFE 5

RESULT 3
Q95M23 PRELIMINARY; PRT; 8 AA.
AC Q95M23;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NA+/K+ ATPASE ALPHA SUBUNIT (EC 3.6.1.37) (FRAGMENT).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIETRAIN;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IIVL genes and
RT linkage assignments of ATP1A1 and IIVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB13B02D3 CRC64;

Query Match 33.3%; Score 15; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TFF 6
Db 6 TVY 8

RESULT 4
Q9ERD2 PRELIMINARY; PRT; 8 AA.
AC Q9ERD2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
```

```
DE GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/D3;
RA Leslie N.D., Bai S.;
RT "Functional analysis of the mouse galactose-1-phosphate uridyl
RT transferase (GALT) promoter.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314226; AAG31161.1; -
KW Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 854 MW; ECBDC409D1ADDD6 CRC64;

Query Match 33.3%; Score 15; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATF 5
Db 3 ATF 5

RESULT 5
Q9R9C2 PRELIMINARY; PRT; 8 AA.
ID Q9R9C2;
AC Q9R9C2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PLASMID cp32-3, POSSIBLE PARTITION PROTEINS (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-3.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022480; AAC35445.1; -
KW Plasmid.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; E8B41B41A735B446 CRC64;

Query Match 31.1%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATF 5
Db 2 NSLYY 6

RESULT 6
Q94VF6 PRELIMINARY; PRT; 8 AA.
ID Q94VF6;
AC Q94VF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus jobiensis.
OG Mitochondrion.
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169843;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407507; AAL10075.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1144 MW; EFD729DB436411A6 CRC64;

Query Match 31.1%; Score 14; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVF 7
Db 4 WYF 6

RESULT 7
ID O09258 PRELIMINARY; PRT; 8 AA.
AC O09258;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DE 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NIPH (FRAGMENT).
GN NIPH.
OS Synecococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synecococcus sp. strain
RT RF-1.";
RL Microbiology 145:743-753(1999).
DR EMBL; AF001780; AAC33369.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
Db 6 FY 7

RESULT 8
ID O87471 PRELIMINARY; PRT; 8 AA.
AC O87471;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DE 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE HIFA (FRAGMENT).
GN HIFA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-EAGAN (EIA);
RX MEDLINE=98389689; PubMed=9721313;
RA Mhlanga-Mutangadura T., Morlin G., Smith A.L., Eisenstark A.,
RA Golomb M.;
RT "Evolution of the major pilus gene cluster of haemophilus
RT influenzae.";
RL J. Bacteriol. 180:4693-4703(1998).
DR EMBL; AF071762; AAC35830.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNA 3
Db 6 NNS 8

RESULT 9
ID Q9TWH6 PRELIMINARY; PRT; 8 AA.
AC Q9TWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DE 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BIOACTIVE PEPTIDE P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllocorida; Nereididae; Perinereis.
OX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95323338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancaurica.";
RL Comp. Biochem. Physiol. C,
RL Pharmacol. Toxicol. Endocrinol. 110:297-304(1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 28.9%; Score 13; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
Db 1 FY 2

RESULT 10
ID O52062 PRELIMINARY; PRT; 8 AA.
AC O52062;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DE 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIGMA FACTOR (FRAGMENT).
GN SPOIIB.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Fawcett P., Melnikov A., Youngman P.;
RT "The Bacillus SPOIGA protein is targeted to sites of sporulation
RT septum formation in a SpoIIE independent manner.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF017181; AAB94056.1; -
DR MEROPS; U04.001; - 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1057 MW; F0D400441B41ADD6 CRC64;

Query Match 26.7%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATF 5
Db 2 ATY 4

RESULT 11
Q49534
ID Q49534 PRELIMINARY; PRT; 8 AA.
AC Q49534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P120 (FRAGMENT).
GN P120.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V2785;
RA Nyvold C., Birkelund S., Christiansen G.;
RT "The Mycoplasma hominis P120 membrane protein gene contains a 659 base pair hypervariable domain."
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22025; AAA67455.1; -
FT NON_TER 1
SQ SEQUENCE 8 AA; 869 MW; 914457605B02C05D CRC64;

Query Match 26.7%; Score 12; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NN 2
Db 7 NN 8

RESULT 12
P82686
ID P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=96010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana."
RL Regul., Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).

CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match 26.7%; Score 12; DB 5; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATF 5
Db 1 DASF 4

RESULT 13
Q34909
ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
OS Locusta migratoria (Migratory locust).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome: RT restriction mapping and sequence of its ND-1(URF-1) gene."
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 26.7%; Score 12; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YFK 8
Db 3 YIK 5

RESULT 14
Q9SB24
ID Q9SB24 PRELIMINARY; PRT; 8 AA.
AC Q9SB24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PARAT PROTEIN (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Niwa Y., Muranaka T., Baba A., Machida Y.;
RT "Organ-specific and auxin-inducible expression of two tobacco para-related genes in transgenic plants."
RL DNA Res. 0:0-0(1994).
DR EMBL; D42119; BAA07700.1; -
FT NON_TER 8

```

SQ SEQUENCE 8 AA; 905 MW; FE32D2C44455BB16 CRC64;

Query Match 26.7%; Score 12; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NN 2
DB 4 NN 5

RESULT 15
Q040659 PRELIMINARY; PRT; 8 AA.
AC Q040659;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALPHA-AMYLASE (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
ON NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomyces
RT cerevisiae."
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.7%; Score 12; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NN 2
DB 5 NN 6

RESULT 16
Q062933 PRELIMINARY; PRT; 8 AA.
AC Q062933;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HISTONE H10 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=TESTIS;
RA Khochbin S., Peretti M.F., Girardot V.;
RT "The structure of differentiation-specific histone H10 gene basal
RT promoter."
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49737; AAA92724.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 850 MW; F4C771B5B44B01A6 CRC64;

Query Match 26.7%; Score 12; DB 11; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TF 5
DB 3 TF 4

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NAT 4
DB 4 NST 6

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
Q15903 PRELIMINARY; PRT; 7 AA.
ID Q15903;
AC Q15903;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE (CLONE XP7E7B) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32082; AAA73893.1; -.
FT NON_TER 7
SQ SEQUENCE 7 AA; 849 MW; 6B040339CDD33DB0 CRC64;

Query Match 24.4%; Score 11; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FK 8
DB 4 FK 5

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18
Q9R5L7 PRELIMINARY; PRT; 8 AA.
ID Q9R5L7;
AC Q9R5L7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
ON NCBI_TaxID=1515;
RN [1]
RP SEQUENCE.
RX MEDLINE=92231850; PubMed=1567379;
RA Romaniec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
RA Demain A.L.;
RT "Purification and characterization of a new endoglucanase from
RT Clostridium thermocellum."
RL Biochem. J. 283:69-73(1992).
SQ SEQUENCE 8 AA; 823 MW; C2CIAB1DD9D1B775 CRC64;

Query Match 24.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TF 5
DB 3 TF 4

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Search completed: July 8, 2002, 11:41:46
Job time: 198 sec

```
RESULT 19
Q9S6D5
ID Q9S6D5 PRELIMINARY; PRT; 8 AA.
AC Q9S6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PUTATIVE IS30 TRANSPOSASE (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Rahn A., Drummelsmith J., Whitfield C.;
RT "Conserved organization in the cps gene clusters for expression of
RT Escherichia coli group 1 K antigens: relationship to the colanic acid
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL J. Bacteriol. 181:2307-2313(1999).
DR EMBL; AF118251; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;
```

Query Match 24.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TF 5
||
Db 4 TF 5

```
RESULT 20
Q9S443
ID Q9S443 PRELIMINARY; PRT; 8 AA.
AC Q9S443;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE BETA-LACTAMASE (FRAGMENT).
GN PSE2.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R545;
RA Roy D., Coulombe M., Perron K., Roy P.H.;
RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
RT gene aac(6')-IIC from the integron of a Chinese Pseudomonas aeruginosa
RT clinical isolate.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162771; AAD46628.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 930 MW; E8DB5DDDD9D1A336 CRC64;
```

Query Match 24.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TF 5
||
Db 3 TF 4

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:37:53 ; Search time 14.17 Seconds
(without alignments)
54.249 Million cell updates/sec

Title: US-09-461-061A-1

Perfect score: 45

Sequence: 1 NNATFFPK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 603

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	35.6	8	2 C61512	variant surface gl
2	16	35.6	8	2 JS0318	leucokinin VIII -
3	15	33.3	7	2 A34026	acetylcholinestera
4	15	33.3	7	2 E33932	Ig mu chain D regi
5	14	31.1	4	2 J01273	neuropeptide Antho
6	14	31.1	7	2 S17976	glucose isomerase
7	14	31.1	8	2 B27867	homeotic protein U
8	13	28.9	3	3 S68328	blood cell protein
9	13	28.9	5	2 P70278	Ig heavy chain CRD
10	13	28.9	8	2 B45800	serum albumin - do
11	13	28.9	8	2 S68325	blood cell protein
12	13	28.9	8	2 A59028	MHC class I histoc
13	12	26.7	5	2 S21077	alpha-amylase - ri
14	12	26.7	5	4 A56077	serawettin W2 - S
15	12	26.7	8	2 B24729	neuropeptide B - b
16	12	26.7	8	2 S70727	ipGF protein - Shi
17	12	26.7	8	2 A14683	aspartate transami
18	11	24.4	4	2 S53508	starvation-induced
19	11	24.4	5	2 S70615	endo-1,4-beta-xyla
20	11	24.4	6	2 S11024	T-cell receptor be
21	11	24.4	6	2 P70650	hydrogensulfite re
22	11	24.4	6	2 A43129	neuropeptide GNFR
23	11	24.4	7	2 S21230	dermorphin (Trp-4,
24	11	24.4	7	2 B35890	RNA-directed DNA p
25	11	24.4	7	2 S33567	tubulin beta-3 cha
26	11	24.4	7	2 P00029	pev-kinin 1 - pena
27	11	24.4	8	2 S08996	hypertrehalosemic
28	11	24.4	8	2 B49823	adipokinetic hormo
29	11	24.4	8	2 B44960	neuropeptide Led-C

30 11 24.4 8 2 A33995 adipokinetic hormo
31 11 24.4 8 2 S11545 adipokinetic hormo
32 11 24.4 8 2 S37141 rpsA protein - Erw
33 11 24.4 8 2 S21273 cellulase (EC 3.2.
34 11 24.4 8 2 S13661 polygalacturonase
35 11 24.4 8 2 A39892 P element, P cytot
36 11 24.4 8 2 PH0803 T-cell receptor al
37 11 24.4 8 2 S65381 cytochrome-c oxida
38 11 24.4 8 2 PC4373 telomeric and tetr
39 10 22.2 4 2 S43014 hypothetical prote
40 10 22.2 5 2 JH0253 R-phycoerythrin ga
41 10 22.2 5 2 JH0253 gut pentapeptide -
42 10 22.2 6 2 A61411 ameleitin - rat
43 10 22.2 6 2 IS1317 BHLH transcription
44 10 22.2 6 2 PT0518 T-cell receptor be
45 10 22.2 6 2 PT0587 T-cell receptor be

ALIGNMENTS

RESULT 1

C61512

variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: C61512

R:Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te

A:Reference number: A61512; MUID:81172836

A:Accession: C61512

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Keywords: glycoprotein

Query Match 35.6%; Score 16; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNA 3

Db 3 NNA 5

RESULT 2

JS0318

leucokinin VIII - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0318

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the

A:Reference number: JS0317

A:Accession: JS0318

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomvotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomvotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 35.6%; Score 16; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ADFY 6

Db 2 ADFY 5

RESULT 3
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C:Accession: A34026
R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; Taylor, J. Biol. Chem. 263, 1140-1145, 1988
A:Title: Divergence in primary structure between the molecular forms of acetylcholinesterase
A:Reference number: A34026; MUID:88087239
A:Accession: A34026
A:Molecule type: protein
A:Residues: 1-7 <GIB>
C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 33.3%; Score 15; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NAT 4
|||
Db 3 NAT 5

RESULT 4
E33932
Ig mu chain D region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
C:Accession: E33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S. Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polypeptide autoantibodies are encoded by nonmutated germ-line
A:Reference number: A33932; MUID:89282853
A:Accession: E33932
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-7 <BAC>
A:Cross-references: GB:M27106
C:Keywords: immunoglobulin

Query Match 33.3%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FYFK 8
|||
Db 3 FYGK 6

RESULT 5
JQ1273
neuropeptide Antho-Kaamide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995
C:Accession: JQ1273
R:Notckner, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P. Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A:Title: Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a novel neuropeptide
A:Reference number: JQ1273; MUID:920282852
A:Accession: JQ1273
A:Molecule type: protein
A:Residues: 1-4 <NOT>
C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following glycosylated
C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation
F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental
F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 31.1%; Score 14; DB 2; Length 4;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YFK 8
|||
Db 1 FFK 3

RESULT 6
S17976
glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)
C:Species: Thermoanaerobacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 17-Apr-1998
C:Accession: S17976
R:Lee, C.; Zeikus, J.G. Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of thermostable glucose isomerase from Clostridium
A:Reference number: S15119; MUID:91144536
A:Accession: S17976
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <LEE>
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having
A:Note: the source is designated as Thermoanaerobacter strain B6A

Query Match 31.1%; Score 14; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YFK 8
|||
Db 4 YFE 6

RESULT 7
B27867
homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 23-Feb-1997
C:Accession: B27867
R:Saari, G.; Bienz, M. EMBO J. 6, 1775-1779, 1987
A:Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.
A:Reference number: A91072
A:Accession: B27867
A:Molecule type: mRNA
A:Residues: 1-8 <SAA>
C:Genetics:
A:Gene: FlyBase:Ubx
A:Cross-references: FlyBase:FBgn0003944
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 31.1%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YFK 8
|||
Db 4 YFE 6

RESULT 8
S68328
blood cell protein A - Molgula manhattensis (fragment)
C:Species: Molgula manhattensis
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: S68328
R:Taylor, S.W.; Ross, M.M.; Waite, J.H. Arch. Biochem. Biophys. 324, 228-240, 1995
A:Title: Novel 3.4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from
A:Reference number: S68325; MUID:96132650

A:Accession: S68328
A:Molecule type: protein
A:Residues: 1-3 <TAY>

Query Match 28.9%; Score 13; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FY 6
||
Db 2 FY 3

RESULT 9

PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0278
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0278
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.9%; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YF 7
||
Db 1 YF 2

RESULT 10

B45800
serum albumin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-1993
C:Accession: B45800
R:Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid protease
A:Reference number: A45800; MUID:89341406
A:Accession: B45800
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <CAR>

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YF 7
||
Db 7 YF 8

RESULT 11

S68325
blood cell protein A8 - Ascidia ceratodes (fragment)
N:Alternate names: Abcp-A
C:Species: Ascidia ceratodes
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
C:Accession: S68325
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995
A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from
A:Reference number: S68325; MUID:96132650
A:Accession: S68325
A:Molecule type: protein
A:Residues: 1-8 <TAY>
F:2,3,4,Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYF 7
||
Db 2 YYY 4

RESULT 12

A59028
MHC class I histocompatibility antigen HLA-C alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001
C:Accession: A59028
R:Escolano, J.M.
submitted to the Protein Sequence Database, August 1998
A:Reference number: A59028
A:Accession: A59028
A:Molecule type: protein
A:Residues: 1-8 <ESC>
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

Query Match 28.9%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YF 7
||
Db 1 YF 2

RESULT 13

S51077
alpha-amylase - rice
C:Species: Oryza sativa (rice)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
C:Accession: S51077
R:Terashima, M.; Kubo, A.; Suzawa, M.; Itoh, Y.; Katoh, S.
Eur. J. Biochem. 226, 249-254, 1994
A:Title: The roles of the N-linked carbohydrate chain of rice alpha-amylase in thermo
A:Reference number: S51077; MUID:95045597
A:Accession: S51077
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <TER>

Query Match 26.7%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNAT 4
||
Db 1 SNGT 4

RESULT 14

A58728
serrawettin W2 - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
C:Accession: A58728

R:Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A:Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and
 A:Reference number: A58728; MUID:92193260
 A:Accession: A58728
 A>Status: unencoded polypeptide
 A:Molecule type: protein
 A:Residues: 1-5 <MAT>

A:Experimental source: strain NS 25
 C:Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
 C:Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded
 F:1/Modified site: D-leucine (Leu) #status experimental
 F:4/Modified site: D-phenylalanine (Phe) #status experimental
 F:1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status expected

Query Match 26.7%; Score 12; DB 4; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATF 5
 :||
 Db 2 STF 4

RESULT 15
 B24749
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
 C:Accession: B24749
 R:Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
 A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
 A:Reference number: A94074; MUID:86067985
 A:Accession: B24749
 A:Molecule type: protein
 A:Residues: 1-8 <YAN>
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide

Query Match 26.7%; Score 12; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYEK 8
 :||
 Db 1 FLFQ 4

RESULT 16
 S70727
 C:Species: Shigella flexneri (fragment)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
 C:Accession: S70727
 R:Allaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Parsc
 Mol. Microbiol. 17, 461-470, 1995
 A:Title: MxiG, a membrane protein required for secretion of Shigella spp. Ipa invasins:
 A:Reference number: S70727; MUID:96100445
 A:Accession: S70727
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-8 <ALL>
 A:Cross-references: EMBL:Z48957; NID:g929880; PIDN:CAA88821.1; PID:g929881
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
 C:Genetics:
 A:Gene: ipgF

Query Match 26.7%; Score 12; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NN 2
 :||
 Db 4 NN 5
 RESULT 17
 A14683
 C:Species: Gallus gallus (chicken)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
 C:Accession: A14683
 R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
 FEBS Lett. 108, 98-102, 1979
 A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
 A:Reference number: A14683; MUID:80092116
 A:Accession: A14683
 A:Molecule type: protein
 A:Residues: 1-8 <WIL>
 C:Keywords: aminotransferase; mitochondrion

Query Match 26.7%; Score 12; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NN 2
 :||
 Db 3 NN 4

RESULT 18
 S53508
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced r
 A:Reference number: S53506; MUID:95201242
 A:Accession: S53508
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <KOE>

Query Match 24.4%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TF 5
 :||
 Db 3 TF 4

RESULT 19
 S70615
 C:Species: Streptomyces sp.
 C:Variety: Chainia sp. NCL 82.5.1
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S70615
 R:Rao, M.; Khadikar, S.; Bandivadekar, K.R.; Deshpande, V.
 Biochem. J. 316, 771-775, 1996
 A:Title: Structural environment of an essential cysteine residue of xylanase from Cha
 A:Reference number: S70615; MUID:96265041
 A:Molecule type: protein
 A:Residues: 1-5 <RAO>

A:Experimental source: Chainia sp. strain NCL 82.5.1
A:Note: the source is designated as Chainia sp.

C:Function:

A:Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans

A:Pathway: fermentation of hemicellulose into ethanol

C:Keywords: glycosidase; hydrolase

Query Match 24.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TF 5

Db 2 TF 3

RESULT 20

S11024

hydrogensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)

N:Alternate names: bisulfite reductase; desulfofuscidin

C:Species: Desulfovibrio thermophilus

C:Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998

C:Accession: S11024

R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; et

al. Biochim. Biophys. Acta 1040, 112-118, 1990

A:Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from

A:Reference number: S11024; MUID:90335276

A:Accession: S11024

A:Molecule type: protein

A:Residues: 1-6 <FAU>

C:Keywords: oxidoreductase

Query Match 24.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FK 8

Db 5 FK 6

Search completed: July 8, 2002, 11:39:07

Job time: 74 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 11:37:48 ; Search time 29.04 Seconds
(without alignments)
30.599 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 69368

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	64.4	8	22	AB55873
2	29	64.4	8	22	AAU28595
3	29	64.4	8	22	AAU24794
4	29	64.4	8	22	AAU26242
5	29	64.4	8	22	AAU15138
6	24	53.3	8	16	AAU73374
7	23	51.1	6	22	AAU08641
8	23	51.1	7	20	AAU40730
9	23	51.1	7	21	AAU30068
10	22	48.9	6	20	AAU23893
11	22	48.9	6	20	AAU97492

12	22	48.9	7	20	AAU23895	Human vascular end
13	21	46.7	4	18	AAW20072	HOX5, a hexose oxi
14	21	46.7	5	17	AAW00431	Interleukin-6 anta
15	21	46.7	6	22	AAU04166	Internal peptide f
16	21	46.7	8	18	AAW11529	Interleukin-6 anta
17	20	44.4	5	19	AAW86298	Rodent IL-1 delta
18	20	44.4	6	20	AAU25842	Human secreted pro
19	20	44.4	6	22	AAU08625	Interleukin-1 inh
20	20	44.4	7	17	AAW94661	GL-7ACA acylase al
21	20	44.4	7	20	AAU40732	S4 derivative #6,
22	20	44.4	7	20	AAU40733	S4 derivative #7,
23	20	44.4	7	21	AAU30070	Scaffold protein S
24	20	44.4	7	21	AAU30071	Scaffold protein S
25	20	44.4	7	22	AAU08638	Interleukin-1 inh
26	20	44.4	8	14	AAU43431	Ro/SSA epitope 47.
27	20	44.4	8	15	AAU61722	PLP peptide 74, po
28	20	44.4	8	16	AAU71815	A.alternata allerg
29	20	44.4	8	22	AAU12635	Human gene 2 encod
30	20	44.4	8	22	AAU08103	Peptide #2 from hu
31	19	42.2	6	16	AAU03970	Cyclic somatostat
32	19	42.2	6	17	AAU08639	Met-enkephalin ana
33	19	42.2	6	17	AAU08636	Met-enkephalin ana
34	19	42.2	6	20	AAU55276	ATCC HB 11885 mono
35	19	42.2	6	21	AAU17213	IL-1 antagonist pe
36	19	42.2	6	21	AAU87022	Human haematopoiet
37	19	42.2	7	15	AAU44688	Somatostatin recep
38	19	42.2	7	16	AAU03971	Cyclic somatostat
39	19	42.2	7	16	AAU03972	Cyclic somatostat
40	19	42.2	7	16	AAU77965	Antigenic Tbp2 pep
41	19	42.2	7	17	AAU90409	Hybridoma ATCC HB-
42	19	42.2	7	18	AAU46158	Predicted antigen
43	19	42.2	7	19	AAU17855	Backbone cyclised
44	19	42.2	7	19	AAU62500	Antibiotic peptide
45	19	42.2	7	19	AAU58754	SEQ ID NO:82 from

ALIGNMENTS

RESULT 1
AB55873
ID AB55873 standard; Peptide; 8 AA.
XX
AC AB55873;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 73.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB01106.
XX
PR 15-MAR-2000; 2000GB-0006285.
PR 24-NOV-2000; 2000GB-0028734.
PR 28-NOV-2000; 2000US-0724391.
XX
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
DR WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy, for
PT comprises analysing body fluid by 2-dimensional electrophoresis, for

PT features correlated with VD -
XX
PS Claim 6; Page 31; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB53801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for
CC monitoring the effect of therapy administered to a subject having VD.
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
CC useful for the treatment of VD and for gene therapy.
XX
SQ Sequence 8 AA;

Query Match 64.4%; Score 29; DB 22; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
||| |||
Db 1 nnahgyfk 8

RESULT 2

AAU28595
ID AAU28595 standard; Peptide; 8 AA.

XX AC AAU28595;

XX 03-JAN-2002 (first entry)

XX DPI tryptic digest peptide #192.

XX Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.

OS Homo sapiens.

PN WO200162787-A1.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00786.

XX 24-FEB-2000; 2000GB-0004412.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective
PT disorder, which is used for diagnosis, prophylaxis and therapy of
PT neuropsychiatric disorders, such as bipolar affective disorder -
XX
PS Disclosure; Page 34; 153pp; English.

XX The present invention relates to the identification of depression
CC associated protein isoforms (DPIs), particularly the tryptic digest
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)

CC described are decreased in the cerebrospinal fluid (CSF) of BAD
CC (bipolar affective disorder) subjects, whilst other DPIs
CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
CC are peptide sequences identified from DPI-45 and DPI-213 and the
CC nucleic acid sequence they are encoded by. The sequences of the
CC invention are useful for clinical screening, diagnosis, prognosis,
CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
CC known as bipolar mood disorder, BP), maniac-depressive illnesses,
CC attention deficit disorders, schizoaffective disorders, and unipolar
CC affective disorders. The present sequence represents one of the DPI
CC tryptic digest peptides of the present invention.

XX SQ Sequence 8 AA;

Query Match 64.4%; Score 29; DB 22; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
||| |||
Db 1 nnahgyfk 8

RESULT 3

AAU24794
ID AAU24794 standard; Peptide; 8 AA.

XX AC AAU24794;

XX 18-DEC-2001 (first entry)

XX Schizophrenia-Associated Protein Isoform (SPI) peptide #23.

XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

OS Homo sapiens.

PN WO200162785-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00792.

XX 24-FEB-2000; 2000GB-0004415.

PR 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570624/64.

XX New schizophrenia associated protein isoforms and encoding nucleic acid
PT molecules, useful for treatment, diagnosis and prognosis of
PT schizophrenia and screening for potential drugs for treatment and new
PT drug targets -

XX Disclosure; Page 29; 148pp; English.

XX The sequence represents a schizophrenia-associated protein isoform (SPI).
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC in cerebrospinal fluid, serum or plasma and are useful markers of
CC schizophrenia. The sequences can be used for treatment and diagnosis of
CC schizophrenia, screening, prognosis, monitoring the results of therapy,
CC identifying patients most likely to respond to a particular therapy and
CC identification of new targets for drug treatment. SPI DNA is useful as a
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX SQ Sequence 8 AA;

Query Match 64.4%; Score 29; DB 22; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
Db 1 nnahgyfk 8

RESULT 4

AAU26242
ID AAU26242 standard; Peptide; 8 AA.

XX AC AAU26242;

XX DT 18-DEC-2001 (first entry)

XX DE Depression-Associated Protein Isoform DPI-205 #3.

XX KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KW CSF; antidepressant; antianemic; nootropic; tranquiliser; neuroleptic;
KW attention deficient disorder; schizoaffective disorder;
KW unipolar affective disorder.

XX OS Homo sapiens.

XX PN WO200163294-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB00791.

XX PR 24-FEB-2000; 2000GB-0004412.

XX PR 08-DEC-2000; 2000GB-0030050.

XX PR 12-DEC-2000; 2000US-0254830.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C;

XX DR WPI; 2001-582081/65.

XX PT Preparation for diagnosing or treating bipolar affected disorder (BAD)

XX PT or unipolar depression, or for screening for modulators, comprises a

XX PS BAD-associated protein isoform -

XX PS Claim 8; Page 34; 163pp; English.

XX CC The invention relates to a preparation comprising an isolated Bipolar
XX CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
XX CC used to screen, diagnose or prognosis of BAD or unipolar depression,
XX CC determine the stage or severity of BAD or unipolar depression, identify a
XX CC subject at risk of developing BAD or unipolar depression, or monitor the
XX CC effect of therapy in a subject. They are also used to screen for or
XX CC identify agents that interact with a DPI. These agents, antibodies
XX CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
XX CC or prevent BAD or unipolar depression. Diseases that can be treated are
XX CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
XX CC unipolar affective disorder. The DPIs are used in proteomics. The
XX CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
XX CC BAD or unipolar depression overcomes the problems of using gene
XX CC expression analysis, such as not being able to obtain central nervous
XX CC system (CNS) tissue from a living patient under normal circumstances.
XX CC The present sequence is a DIP decreased in the CSF (cerebro-spinal
XX CC fluid) of subjects having BAD.

XX Sequence 8 AA;

Query Match 64.4%; Score 29; DB 22; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
Db 1 nnahgyfk 8

RESULT 5

AAU15138
ID AAU15138 standard; Peptide; 8 AA.

XX AC AAU15138;

XX DT 24-OCT-2001 (first entry)

XX DE Schizophrenia-associated isoform peptide #23.

XX KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.

XX OS Homo sapiens.

XX PN WO200163293-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB00783.

XX PR 24-FEB-2000; 2000GB-0004415.

XX PR 28-NOV-2000; 2000US-0750395.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C;

XX DR WPI; 2001-502868/55.

XX PT Diagnosing and monitoring Schizophrenia by detecting the presence of
XX PT Schizophrenia Associated Features and Schizophrenia Associated Protein
XX PT isoforms in samples of cerebrospinal fluid -

XX PS Claim 6; Page 29; 160pp; English.

XX CC The invention relates to methods and compositions for screening,
XX CC diagnosis and prognosis of Schizophrenia. The method involves detecting
XX CC the presence of Schizophrenia (SCH) Associated features (Sfs) and SCH
XX CC Associated Protein Isoforms (SPis) in samples, e.g. by electrophoresis,
XX CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
XX CC studying the effectiveness of treatments and for identifying potential
XX CC therapeutic agents. The method is used for (1) screening or diagnosis of
XX CC SCH and the relative abundance of at least 1 chosen feature correlates
XX CC with the presence or absence of SCH; and (2) monitoring the effect of
XX CC therapy administered to a subject with SCH and the relative abundance of
XX CC at least 1 chosen feature which correlates with the severity of SCH.
XX CC The expression and activity of the Sfs, SPis and related molecules
XX CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
XX CC progress of the disorder and the effectiveness of treatment and as
XX CC targets to identify and produce potential therapeutic agents for the
XX CC treatment of SCH. The paucity of detectable neuroalgalic defects
XX CC distinguishes neuropsychiatric disorders such as SCH from neurological
XX CC disorders, where manifestations of anatomical and biochemical changes
XX CC have been identified in many cases. Consequently the identification and
XX CC characterisation of cellular and/or molecular causative defects and
XX CC neuropathies are necessary for improved treatment of neuropsychiatric
XX CC disorders. AAU15114-AAU15762 represent the amino acid sequences of
XX CC Schizophrenia-associated isoforms used in the method of the invention.

XX Sequence 8 AA;

Query Match 64.4%; Score 29; DB 22; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYK 8
 ||| |||
 Db 1 nnahgyfk 8

RESULT 6
 AAR73374
 ID AAR73374 standard; Peptide; 8 AA.
 XX
 AC AAR73374;
 XX
 DT 08-DEC-1995 (first entry)
 XX
 DE Human TSH receptor (residues 347-354).
 XX
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
 KW antibody; affinity; detection.
 XX
 OS Synthetic.
 XX
 PN JP07089991-A.
 XX
 PD 04-APR-1995.
 XX
 PF 28-SEP-1993; 93JP-0240853.
 XX
 PR 28-SEP-1993; 93JP-0240853.
 XX
 PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 DR WPI; 1995-167251/22.
 XX
 PT Novel polypeptide(s) having affinity for the human TSH receptor
 PT antibody - used in detection of the TSH antibody.
 XX
 PS Example 1; Page 28; 54pp; Japanese.
 XX
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC AAR73201-592).
 XX
 XX Sequence 8 AA;

Query Match 53.3%; Score 24; DB 16; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFY 6
 ||| :|
 Db 2 nnahy 7

RESULT 7
 AAU08641
 ID AAU08641 standard; Peptide; 6 AA.
 XX
 AC AAU08641;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Interleukin-1 inhibitor based peptide #5.
 XX
 KW Interleukin-1 inhibitor; IL-1i; antiarthritic;
 KW antirheumatic; antiulcer; osteopathic; antidiabetic; antipsoriatic;
 KW immunosuppressive; antigout; antiinflammatory; rheumatoid arthritis;
 KW Crohn's disease; ulcerative colitis; osteoporosis; juvenile diabetes;
 KW psoriasis; lupus erythematosus; fibrosis; glomerulonephritis; gout;
 KW acute febrile illness; sarcoidosis; lymphoma; vascular occlusion;
 KW interstitial lung disease.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "Encoded by AAYCARARACNTTYTA"
 XX
 PN EPI133995-A2.
 XX
 PD 19-SEP-2001.
 XX
 PE 26-MAY-1989; 2001EP-0107950.
 XX
 PR 27-MAY-1988; 88US-0199915.
 PR 31-AUG-1988; 88US-0238713.
 PR 23-SEP-1988; 88US-0248521.
 PR 03-NOV-1988; 88US-0266531.
 PR 26-MAY-1989; 89EP-0109540.
 PR 26-MAY-1989; 92EP-0114773.
 XX
 PA (SYND) SYNERGEN INC.
 XX
 XX Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG;
 PI Sommer A;
 XX
 DR WPI; 2001-566880/64.
 DR N-PSDB; AASI3435.
 XX
 PT Recombinant interleukin-1 inhibitors and polynucleotides encoding the
 PT protein useful for treating an IL-1 mediated pathophysiological
 PT condition which includes arthritis, rheumatoid arthritis, Crohn's
 PT disease -
 XX
 PS Example 6; Page 22; 58pp; English.
 XX
 CC The invention relates to a recombinant polypeptide having interleukin-1
 CC inhibitor (IL-1i) activity against IL-lalpha, IL-lbeta or both.
 CC The IL-1i is useful for preparing pharmaceutical composition for
 CC treating an IL-1 mediated pathophysiological condition which includes
 CC arthritis, rheumatoid arthritis, Crohn's disease, ulcerative colitis,
 CC osteoporosis, juvenile diabetes, psoriasis, lupus erythematosus,
 CC fibrosis, glomerulonephritis, gout, acute febrile illness, sarcoidosis,
 CC lymphomas, a patient after damage to the brain from vascular occlusion,
 CC or acute or chronic interstitial lung disease. The present sequence
 CC is a peptide based on an IL-1i of the invention, used to design
 CC degenerate probes for isolating nucleic acids encoding IL-1i molecules.
 XX
 XX Sequence 6 AA;

Query Match 51.1%; Score 23; DB 22; Length 6;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFY 6
 | |||
 Db 1 nqktfy 6

RESULT 8
 AAY40730
 ID AAY40730 standard; peptide; 7 AA.
 XX
 AC AAY40730;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE S4 derivative #4, beta strand of scaffold protein structure.
 XX
 KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
 KW tumour; chemotherapeutic agent.
 XX
 OS Synthetic.
 XX
 PN EP947582-A1.

XX 06-OCT-1999.
PD 31-MAR-1998; 98EP-0870065.
XX 31-MAR-1998; 98EP-0870065.
XX (INNO-) INNOGENETICS NV.
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
PI WPI; 1999-542958/46.
XX New scaffold protein, useful for stabilizing antigens used as vaccines
PT
XX Disclosure; Page 6; 105pp; English.
XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.
XX
XX Sequence 7 AA;
SQ

Query Match 51.1%; Score 23; DB 20; Length 7;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TFYFK 8
Dd ||| |
3 tfylk 7

RESULT 9
AAB30068
ID AAB30068 standard; Peptide; 7 AA.
XX
AC AAB30068;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 129.
XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX Synthetic.
OS
XX WO200060070-A1.
PN
XX

PD 12-OCT-2000.
XX 01-APR-1999; 99WO-EP02283.
XX 01-APR-1999; 99WO-EP02283.
XX (INNO-) INNOGENETICS NV.
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
PI WPI; 2000-665002/64.
XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments -
XX
XX Disclosure; Page 15; 68pp; English.
XX The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB29930-B29939 were used in the
CC production of the proteins of the invention.
XX
XX Sequence 7 AA;
SQ

Query Match 51.1%; Score 23; DB 21; Length 7;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TFYFK 8
Dd ||| |
3 tfylk 7

RESULT 10
AAY23893
ID AAY23893 standard; Peptide; 6 AA.
XX
AC AAY23893;
XX
DT 21-SEP-1999 (first entry)
XX
DE Human vascular endothelial growth factor (VEGF)-D derived peptide.
XX
KW Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
XX Homo sapiens.
OS
XX WO9933485-A1.
PN
XX 08-JUL-1999.
PD
XX 23-DEC-1998; 98WO-US27373.
PF
XX 29-MAY-1998; 98US-0087392.
PR
XX 24-DEC-1997; 97AU-0001131.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Achen MG, Alitalo K, Stackner SA;
PI
XX WPI; 1999-405368/34.
DR
XX A human cell line stably expressing vascular endothelial growth
PT factor D, useful for treating melanomas or tumours expressing VEGF-D
XX

Example 7; Page 75; 79pp; English.

PS The present sequence is derived from vascular endothelial growth
XX factor (VEGF)-D. The specification describes a human cell line
CC which stably expresses VEGF-D, or fragments/analogs having VEGF-D
CC biological activity. VEGF-D antagonists, e.g. antisense nucleic acids
CC or triplex DNA, VEGF-D variants or antibodies (especially chimeric
CC antibodies), are useful for the treatment or alleviation of malignant
CC melanomas, tumours or psoriasis. Angiogenesis and lymphangiogenesis
CC stimulating amounts of VEGF-D can be administered to enhance the
CC acceptance and/or healing of skin grafts or to stimulate the healing
CC of a surgical or traumatic wound to the skin. Lymphangiogenesis
CC stimulating amounts of VEGF-D can be used to treat lymphedema.
CC Endothelial proliferation stimulating amounts of VEGF-D are used to
CC treat scleroderma. Vascularisation stimulating amounts of VEGF-D can
CC be used to treat anhydrotic ectodermal dysplasia. VEGF-D antibodies are
CC useful for detecting tumours expressing VEGF-D. Fully-processed VEGF-D
CC can be used to stimulate at least one VEGF-D bioactivity chosen from
CC endothelial cell proliferation, migration, survival and differentiation
CC and lymphangiogenesis without inducing vascular permeability.
XX
SQ

Sequence 6 AA;

Query Match 48.9%; Score 22; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATFF 6
|||
Db 3 atfy 6

RESULT 11

AAW97492
ID AAW97492 standard; peptide; 6 AA.

AC AAW97492;

DT 19-MAY-1999 (first entry)

DE Antigenic site of HN protein loop beta-3L01.

XX Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX Bovine parainfluenza virus.

OS WO9902695-A2.

PN 21-JAN-1999.

PD 08-JUL-1998; 98WO-NL00390.

PF 08-JUL-1997; 97EP-0202100.

XX (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

PA Langedijk JPM, Van Oirschot JT;

PI WPI; 1999-120896/10.

DR Isolated proteinaceous substance - comprising at least one virus
XX epitope derived from an attachment protein of a paramyxovirus

PS Disclosure; Page 45; 63pp; English.

XX AAW97452-571 represent antigenic sites derived from the
CC haemagglutinin-neuraminidase (HN) protein of the paramyxoviridae.
CC The specification describes 3-D models identifying a proteinaceous
CC substance comprising at least one virus epitope derived from the
CC attachment protein, which corresponds to an antigenic site present on
CC one of the loops of HN. The antigenic sites can be used to produce

CC vaccines, to detect the viruses, and to select the immunodominant
XX epitope.

SQ Sequence 6 AA;

Query Match 48.9%; Score 22; DB 20; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATF 5
|||
Db 1 nnitf 5

RESULT 12

AAV23895
ID AAY23895 standard; Peptide; 7 AA.

XX AAY23895;

XX 21-SEP-1999 (first entry)

DE Human vascular endothelial growth factor (VEGF)-D derived peptide.

XX Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
KW tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
KW wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.

XX Homo sapiens.

XX WO9933485-A1.

XX 08-JUL-1999.

PF 23-DEC-1998; 98WO-US27373.

XX 29-MAY-1998; 98US-0087392.

PR 24-DEC-1997; 97AU-0001131.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Alitalo K, Stacker SA;

XX WPI; 1999-405368/34.

XX A human cell line stably expressing vascular endothelial growth
PT factor D, useful for treating melanomas or tumours expressing VEGF-D

XX Example 7; Page 75; 79pp; English.

XX The present sequence is derived from vascular endothelial growth
CC factor (VEGF)-D. The specification describes a human cell line
CC which stably expresses VEGF-D, or fragments/analogs having VEGF-D
CC biological activity. VEGF-D antagonists, e.g. antisense nucleic acids
CC or triplex DNA, VEGF-D variants or antibodies (especially chimeric
CC antibodies), are useful for the treatment or alleviation of malignant
CC melanomas, tumours or psoriasis. Angiogenesis and lymphangiogenesis
CC stimulating amounts of VEGF-D can be administered to enhance the
CC acceptance and/or healing of skin grafts or to stimulate the healing
CC of a surgical or traumatic wound to the skin. Lymphangiogenesis
CC stimulating amounts of VEGF-D can be used to treat lymphedema.
CC Endothelial proliferation stimulating amounts of VEGF-D are used to
CC treat scleroderma. Vascularisation stimulating amounts of VEGF-D can
CC be used to treat anhydrotic ectodermal dysplasia. VEGF-D antibodies are
CC useful for detecting tumours expressing VEGF-D. Fully-processed VEGF-D
CC can be used to stimulate at least one VEGF-D bioactivity chosen from
CC endothelial cell proliferation, migration, survival and differentiation
CC and lymphangiogenesis without inducing vascular permeability.

XX Sequence 7 AA;

Query Match 48.9%; Score 22; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATFY 6
Db 4 atfy 7

RESULT 13
AAW20072
ID AAW20072 standard; peptide: 4 AA.
XX AC AAW20072;
XX DF 12-SEP-1997 (first entry)
XX DE HOX5, a hexose oxidase derived antimicrobial/antioxidant peptide.
XX KW Hexose oxidase; Chondrus crispus; marine algae; recombinant;
KW antimicrobial; antioxidant; food preparation; dairy product; starch;
KW beverage; animal feed; silage; sugar reduction; cosmetics; dental;
KW toothpaste; dough; lactone production.
XX OS Chondrus crispus.
XX PN W09640935-A1.
XX PD 19-DEC-1996.
XX PF 04-JUN-1996; 96WO-DK00238.
XX PR 07-JUN-1995; 95US-0476910.
XX PA (BIOT-) BIOTEKNOLOGISK INST.
XX PI Hansen OC, Stougaard P;
XX DR WPI; 1997-052333/05.
XX PT Recombinant production of polypeptide having hexose oxidase activity
PT - used in food preparations as antibacterial and antioxidant agent
XX PS Claim 6; Page 100; 124pp; English.
XX CC AAW20068-75 are small peptides derived from hexose oxidase (HO) of the
CC marine algae species Chondrus crispus. Hexose oxidase and peptides
CC having HO activity are useful in the production of food products, e.g.
CC dairy products, starch-containing food products (dough) and non-dairy
CC beverages. HO and active peptide fragments have antimicrobial and
CC antioxidant properties and act by removing all the oxygen in a food
CC packaging. HO and peptides of HO can also be used in an animal feed,
CC especially silage. Further uses are to reduce, or analyse, the sugar
CC content in a food, in the production of cosmetics, tooth care products
CC or a pharmaceutical product and in lactone production. HO can be
CC recombinantly produced in industrially appropriate quantities, and at
CC a quality and purity level which renders polypeptide suitable for
CC industrial purposes.
XX SQ Sequence 4 AA;

Query Match 46.7%; Score 21; DB 18; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYFK 8
Db 1 yyfk 4

RESULT 14
AAW00431

Query Match 46.7%; Score 21; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFY 6
Db 1 nssfy 5

RESULT 15
AAB04166
ID AAB04166 standard; Peptide; 6 AA.
XX AC AAB04166;
XX DF 11-APR-2001 (first entry)
XX DE Internal peptide fragment of fructosyl transferase.
XX KW Fructan exohydrolase; FEH; transgenic plant; recombination;
KW transgene; gene expression; detergent; detergent additive;
KW oral care composition.
XX OS Cichorium intybus.
XX PN W0200068402-A1.
XX PD 16-NOV-2000.
XX PF 08-MAY-2000; 2000WO-EP04226.
XX PR 06-MAY-1999; 99BE-0000329.

ID AAW00431 standard; peptide; 5 AA.
XX AC AAW00431;
XX DT 29-AUG-1996 (first entry)
XX DE Interleukin-6 antagonist peptide.
XX KW IL-6; antagonist; autoimmune disease.
XX OS Synthetic.
XX PN JP07324097-A.
XX PD 12-DEC-1995.
XX PF 30-MAY-1994; 94JP-0117259.
XX PR 30-MAY-1994; 94JP-0117259.
XX PA (DAIL) DAICEL CHEM IND LTD.
XX PA (FUJI) FUJISAWA PHARM CO LTD.
XX DR WPI; 1996-065476/07.
XX PT Interleukin 6 antagonist - useful for treating autoimmune diseases
XX PS Claims 4, 6; Pages 2, 3; 19pp; Japanese.
XX CC New IL-6 antagonists are provided which are of formula X-W-Y, in
CC which X is H or an amino-protecting group, Y is OH or a carboxy-
CC protecting group, and W is a peptide containing all or part of the
CC sequence as given in AAW00401, AAW00402, AAW00403 or AAW00404, where any
CC free mercapto groups in the sequence are optionally protected. The
CC present sequence is a specifically preferred partial sequence of AAW00403
CC and is itself claimed as a new chemical entity.
XX CC The IL-6 antagonists are useful for treating autoimmune diseases.
XX SQ Sequence 5 AA;

Query Match 46.7%; Score 21; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFY 6
Db 1 nssfy 5

RESULT 15
AAB04166
ID AAB04166 standard; Peptide; 6 AA.
XX AC AAB04166;
XX DF 11-APR-2001 (first entry)
XX DE Internal peptide fragment of fructosyl transferase.
XX KW Fructan exohydrolase; FEH; transgenic plant; recombination;
KW transgene; gene expression; detergent; detergent additive;
KW oral care composition.
XX OS Cichorium intybus.
XX PN W0200068402-A1.
XX PD 16-NOV-2000.
XX PF 08-MAY-2000; 2000WO-EP04226.
XX PR 06-MAY-1999; 99BE-0000329.

XX PA (LEUV-) LEUVEN RES & DEV.
 XX PS Van Den Ende W, Van Laere A, De Roover J, Michiels A;
 XX PI WPT; 2001-007401/01.
 XX DR Novel DNA molecules encoding enzymes having fructan exohydrolase
 XX PT activity for use in transgenic plant production, dental care
 XX PT compositions, and in detergents
 XX PS Example 1; Page 16; 45pp; English.
 XX CC Transgenic plants such as Cichoraria intybus, Cynara scolymus,
 CC Helianthus tuberosus, Scorzonera hispanica, Oryza sativa, Zea mays,
 CC Triticum aestivum, Triticum durum, Hordeum vulgare, Secale cereale,
 CC Avena sativa, Sorghum vulgare, Phleum pratense, Lolium temulentum,
 CC Dactylis glomerata, Pennisetum americanum, Allium cepa, Agave
 CC americanum, Agave azul tequilana, Sorghum bicolor and Panicum milaceum,
 CC transformed with a vector encoding a fructan exohydrolase (FEH)
 CC enzyme are useful for the recombinant production of FEH or other
 CC polypeptides having FEH activity. The FEH polypeptides produced
 CC are useful in detergents or as a detergent additive and in oral
 CC care compositions. This internal conserved peptide sequence of
 CC fructosyl transferase and invertase was used to create a
 CC degenerate antisense primer for amplifying the FEH coding sequence.
 XX SQ Sequence 6 AA;

Query Match 46.7%; Score 21; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNAT 4
 Db 2 nnat 5

RESULT 16
 AAW11529
 ID AAW11529 standard; peptide; 8 AA.
 XX AC AAW11529;
 XX DT 22-APR-1997 (first entry)
 XX DE Interleukin-6 antagonist 2.
 XX KW Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease;
 KW skin; intestine; systemic lupus erythematosus; chronic rheumatism.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 8 /note= "amidated"
 FT XX
 XX PN JP08311098-A.
 XX PD 26-NOV-1996.
 XX PF 22-MAY-1995; 95JP-0146742.
 XX PR 22-MAY-1995; 95JP-0146742.
 XX PA (DAIL) DAICEL CHEM IND LTD.
 XX PA (FUJI) FUJISAWA PHARM CO LTD.
 XX DR W&A; 1997-061811/06.
 XX PT Interleukin-6 antagonistic peptide(s) comprising arginine - useful
 PT for treating autoimmune, renal, skin and intestinal diseases

XX PS Example 2; Page 11; 20pp; Japanese.
 XX CC The present peptide is a specific example of new interleukin-6
 CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino
 CC acids or an amino group protecting group; Y is 1-5 amino acids, a
 CC carboxyl group protecting group or an amide; A is preferably Arg
 CC having an opt. protected guanidino group but can be any amino acid;
 CC D is Arg having an opt. protected guanidino group and B is preferably
 CC a Leu residue but can be any amino acid, including non-natural
 CC amino acids, opt. having a protected side-chain. The peptides are
 CC useful for treating autoimmune diseases (e.g. systemic lupus
 CC erythematosus or chronic rheumatism), renal, skin and intestinal
 CC diseases.
 XX SQ Sequence 8 AA;

Query Match 46.7%; Score 21; DB 18; Length 8;
 Best Local Similarity 60.0%; Pred. No. 6.4e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFY 6
 Db 1 nssfy 5

RESULT 17
 AAW86298
 ID AAW86298 standard; peptide; 5 AA.
 XX AC AAW86298;
 XX DT 19-FEB-1999 (first entry)
 XX DE Rodent IL-1 delta polypeptide fragment (residues 150-154).
 XX KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
 KW inflammatory response; immune system; diagnosis; agonist; antagonist;
 XX chemokine.
 XX OS Mus sp.
 XX PN WO9847921-A1.
 XX PD 29-OCT-1998.
 XX PF 17-APR-1998; 98WO-US06879.
 XX PR 06-AUG-1997; 97US-0055111.
 XX PR 21-APR-1997; 97US-0837627.
 XX PA (SCHE) SCHERING CORP.
 XX PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;
 XX DR WPI; 1998-609976/51.
 XX PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
 XX PT regulating the immune system and inflammatory responses
 XX PS Claim 1; Page 99; 113pp; English.
 XX CC The invention relates to a recombinant polypeptide that specifically
 CC binds polyclonal antibodies (Abs) generated against a 12 consecutive
 CC amino acid segment of interleukin (IL)-1 delta or IL-1 epsilon. Agonists
 CC or antagonists of these IL polypeptides are used to regulate a cell
 CC involved in an inflammatory response. The IL-1 delta or IL-1 epsilon
 CC polypeptides and peptides are used to produce Abs and antigen-Abs
 CC complexes. The polypeptides, Abs and the corresponding nucleic acids
 CC regulate development and/or the immune system, and can be used to
 CC diagnose and treat conditions associated with abnormal expression of IL.
 CC Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are

CC used with agonists or antagonists of IL-1 alpha, IL-1RA, IL-1 beta, IL-1
 CC gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon polypeptides
 CC may be used as a soluble polypeptide or as a fusion protein with another
 CC cytokine or chemokine. Sequences AA86287 to AA86300 represent peptide
 CC fragments of a rodent interleukin (IL)-1 delta polypeptide.
 XX
 SQ Sequence 5 AA;

Query Match 44.4%; Score 20; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 6.4e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FYFK 8
 |||
 Db 1 fyfq 4

RESULT 18
 AAY25842
 ID AAY25842 standard; Protein; 6 AA.

XX AC AAY25842;

XX DT 04-OCT-1999 (first entry)

XX DE Human secreted protein fragment encoded from gene 49.

XX KW Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour;
 KW neurodegenerative disorder; developmental abnormality; blood disorder;
 KW fetal deficiency; blood disorder; leukemia; immune system; inflammation;
 KW autoimmune disease; hepatic disease; renal disease; allergy; restenosis;
 KW ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;
 KW cardiovascular disorder; wound healing; stroke; arthritis; obesity;
 KW asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;
 KW metabolic disorder.

XX OS Homo sapiens.

XX PN WO9938881-A1.

XX PD 05-AUG-1999.

XX PF 27-JAN-1999; 99WO-US01621.

XX PR 30-JAN-1998; 98US-00731170.

XX PR 30-JAN-1998; 98US-00731159.

XX PR 30-JAN-1998; 98US-00731160.

XX PR 30-JAN-1998; 98US-00731161.

XX PR 30-JAN-1998; 98US-00731162.

XX PR 30-JAN-1998; 98US-00731164.

XX PR 30-JAN-1998; 98US-00731165.

XX PR 30-JAN-1998; 98US-00731167.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Carter KC, Endress GA, Feng P, Ferrie AM, Florence C;

XX PI Florence KA, Janat F, NI J, Rosen CA, Ruben SM;

XX PI Soppet DR, Young P, Yu G;

XX DR WPI; 1999-469315/39.

XX DR N-PSDB; AA200458.

XX PT New isolated human genes and the secreted polypeptides they encode

XX PS useful in, e.g. treatment of Alzheimer's

XX PS Disclosure; Page 365; 393pp; English.

XX CC This invention describes novel human genes (see AA200410-200477) and the
 CC secreted proteins (see AAY25711-Y25778) and fragments (see
 CC AAY25779-Y25907) they encode. The polynucleotides and their corresponding
 CC secreted polypeptides are useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. Also pathological

CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 67
 CC polynucleotides of the invention, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis
 CC or treatment of cancer, tumours, neurodegenerative disorders,
 CC developmental abnormalities and fetal deficiencies, blood disorders,
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic
 CC and renal disease, inflammation, allergies, ischaemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, restenosis, cardiovascular
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners.

XX SQ Sequence 6 AA;

Query Match 44.4%; Score 20; DB 20; Length 6;
 Best Local Similarity 66.7%; Pred. No. 6.4e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 ATFYFK 8

Db 1 arvyfk 6

RESULT 19

AAU08625

ID AAU08625 standard; Peptide; 6 AA.

XX AC AAU08625;

XX DT 18-DEC-2001 (first entry)

XX DE Interleukin-1 inhibitor IL-11-a (RalphalysC-31).

XX KW Interleukin-1 inhibitor; IL-11-a; RalphyLysC-31; antiarthritic;

XX KW antirheumatic; antiulcer; osteopathic; antidiabetic; antipsoriatic;

XX KW immunosuppressive; antigout; antinflammatory; rheumatoid arthritis;

XX KW Crohn's disease; ulcerative colitis; osteoporosis; juvenile diabetes;

XX KW psoriasis; lupus erythematosus; fibrosis; glomerulonephritis; gout;

XX KW acute febrile illness; sarcoidosis; lymphoma; vascular occlusion;

XX KW interstitial lung disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN EPI133995-A2.

XX PD 19-SEP-2001.

XX PF 26-MAY-1989; 2001EP-0107950.

XX PR 27-MAY-1988; 88US-0199915.

XX PR 31-AUG-1988; 88US-0238713.

XX PR 23-SEP-1988; 88US-0248521.

XX PR 03-NOV-1988; 88US-0266531.

XX PR 26-MAY-1989; 89EP-0109540.

XX PR 26-MAY-1989; 92EP-0114773.

XX PA (SYND) SYNERGEN INC.

XX PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG;

XX PI Sommer A;

XX XX WPI; 2001-566880/64.

XX PT Recombinant interleukin-1 inhibitors and polynucleotides encoding the
 XX protein useful for treating an IL-1 mediated pathophysiological
 XX condition which includes arthritis, rheumatoid arthritis, Crohn's
 XX disease

PS Example 3; Page 19; 58pp; English.

XX The invention relates to a recombinant polypeptide having interleukin-1
CC inhibitor (IL-1i) activity against IL-1alpha, IL-1beta or both.
CC The IL-1i is useful for preparing pharmaceutical composition for
CC treating an IL-1 mediated pathological condition which includes
CC arthritis, rheumatoid arthritis, Crohn's disease, ulcerative colitis,
CC osteoporosis, juvenile diabetes, psoriasis, lupus erythematosus,
CC fibrosis, glomerulonephritis, gout, acute febrile illness, sarcoidosis,
CC lymphomas, a patient after damage to the brain from vascular occlusion,
CC or acute or chronic interstitial lung disease. The present sequence
CC is an IL-1i of the invention.

XX Sequence 6 AA;

Query Match 44.4%; Score 20; DB 22; Length 6;

Best Local Similarity 75.0%; Pred. No. 6.4e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8

Db 1 fyfq 4

RESULT 20

AAW94661

ID AAW94661 standard; peptide; 7 AA.

XX AC AAW94661;

XX DT 30-APR-1999 (first entry)

XX DE GL-7ACA acylase alternative N-terminal peptide #3.

XX KW 7-beta-(4-carboxybutanamido)-cephalosporanic acid acylase;

XX KW GL-7ACA acylase; 7-amino-cephalosporin; cephalosporin.

XX OS Synthetic.

XX PN JP07313161-A.

XX PD 05-DEC-1995.

XX PF 24-MAY-1994; 94JP-0110066.

XX PR 24-MAY-1994; 94JP-0110066.

XX PA (FUJI) FUJISAWA PHARM CO LTD.

XX DR WPT; 1996-053784/06.

XX PT New carboxy:butanamido-cephalosporanic acid acylase - prepd by
PT recombinant DNA methods, used for prepn of 7-amino-cephalosporin
PT cpds

XX PS Claim 1; Page 2; 18pp; Japanese.

XX The present invention describes 7-beta-(4-carboxybutanamido)-
CC cephalosporanic acid acylase (GL-7ACA acylase) which has an amino acid
CC sequence in which part of the N-terminal sequence of natural GL-7ACA
CC acylase is replaced by at least one amino acid sequence selected from
CC AAW94659 to AAW94663. The GL-7ACA acylases of the present invention can
CC be prepared in a large amount and they are useful for the commercial
CC production of cephalosporin compounds.

XX Sequence 7 AA;

Query Match

Best Local Similarity 44.4%; Score 20; DB 17; Length 7;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYFK 8

Db 2 fyfe 5

Search completed: July 8, 2002, 11:38:27

Job time: 39 sec



Creation date: 02-10-2004
Indexing Officer: THAILEMARIAM - TIZITA HAILEMARIAM
Team: OIPEBackFileIndexing
Dossier: 09461061

Legal Date: 07-10-2002

No.	Doccode	Number of pages
1	SRNT	40

Total number of pages: 40

Remarks:

Order of re-scan issued on

